IDC DOCUMENTATION

Radionuclide Software User Manual

Revision 2

Notice

This document was published by the NBC Defense Systems Group of Veridian as part of the International Data Centre (IDC) Documentation. It was first published in March 1999 and was republished electronically as Revision 1 in November 2001 and Revision 2 in December 2001 to include major changes. IDC documents that have been changed substantially are indicated by a whole revision number (for example, Revision 1).

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Ordering Information

The ordering number for this document is PSR-00/TN2874.

This document is cited within other IDC documents as [IDC6.5.10Rev2].

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About this Document

PURPOSE

This document describes how to use the Radionuclide software of the International Data Center (IDC) and is identified as the *Radionuclide Software User Manual, Revision 2,* [IDC6.5.10Rev2].

This document supersedes the information contained in the *Radionuclide Software User Manual Revision 1*, published November 2001, and provides new and revised instructions that incorporate new features of the software.

SCOPE

This document is part of the overall documentation architecture for the International Data Center and includes task-oriented instructions on how to set up the software and use its features. The information is modeled on the Data Item Description for Software User Manuals [DOD94a] and other industry standards. This document does not describe software design and requirements or provide instructions for installing the software. These topics are described in sources cited in "Related Information."

AUDIENCE

This document is oriented to the first-time or occasional user of the software. However, more experienced users may find certain sections useful as a reference.

RELATED INFORMATION

The following documents complement this document

- *Database Schema* [IDC5.1.1Rev2]

- *IDC Processing of Radionuclide Data* [IDC5.2.2Rev1]
- Radionuclide Software Design [IDC 7.1.10Rev1]

See “References” on page 239 for a listing of the references consulted in preparing this document.

USING THIS DOCUMENT

Most chapters in this document progress from high-level descriptions of the software’s capabilities and operating environment to instructions on getting started and using the software features. If you are a new user of the software, read the Introduction and Procedures for the software components of interest in sequential order. If you are an experienced user of the software, you can randomly access information to review procedures for particular tasks or to solve problems. Use the Table of Contents to find a specific task or skim through the headings in the applicable chapter.

This document uses graphical, typographical, and naming conventions, as described in the following tables:

TABLE I: TYPOGRAPHICAL CONVENTIONS

Element	Font	Example
database table	**bold**	**dataready**
database table and attribute when written in the dot notation		**prodtrack.***status*
headings, figure titles, and table titles		About this Document
database columns	*italics*	*status*
processes, software units, and libraries		*ParseSubs*
titles of documents		*Subscription Subsystem Software*
computer code and output	`courier`	`>(list ‘a ‘b ‘c)`
filenames, directories, and websites		`messages@pidc.org`
text that should be typed in exactly as shown		`edit-filter-dialog`

TABLE II: KEYBOARD, COMMAND, AND MENU CONVENTIONS

Instruction	Explanation	Example
choose	Use keyboard shortcuts or click once with your (left) mouse to select a menu option.	Choose File>Print.
click	Press and release your (left) mouse button to activate a button on the screen.	Click Send in the dialog box.
double-click	Click a mouse button twice without moving the pointer.	Double-click the Maximize icon to reopen the program.
drag	Hold down the (left) mouse button while moving the pointer.	Drag the pointer to draw a rectangle around the region of interest.
key-key	Indicates simultaneous key strokes. Hold down the first key and press the second key.	control-e (Hold down the control key and press the letter e.)
key, key	Indicates consecutive keystrokes. Press the first key, release it, then press the second key.	esc,v (Press the esc key, release it, then press the letter v.)
menu>submenu	Choose (submenu) from (menu).	File>Print (Choose Print from the File menu.)
pointer	Move the mouse without pressing the (left) mouse button. The mouse appears as a pointer (arrow) on the inactive portions of your screen. The pointer becomes a cursor and the area becomes active when you click the mouse button.	Drag the pointer to draw a rectangle around the region of interest.
press	Press a key or sequence of keys or hold down the left mouse button.	Press the enter key.

TABLE II: KEYBOARD, COMMAND, AND MENU CONVENTIONS

Instruction	Explanation	Example
pull-down menu	A list of options related to a menu. The list appears as long as you press on the related menu.	Choose a year from the Date pull-down menu.
select	Highlight or click on data.	Select the text to be copied. Select a waveform.
toggle	Turn a particular mode on or off by clicking a button or key.	Use the Line Style toggle button to switch between gird modes.

▼ About this Document

Chapter 1: Introduction

This chapter provides a general description of the software and includes the following topics:

- Overview
- Status of Development
- Functionality
- Operations

Chapter 1: Introduction

OVERVIEW

The IDC software acquires time series and radionuclide data from stations of the International Monitoring System (IMS) and other locations. These data are passed through a number of automatic and interactive analysis stages, resulting in a location estimate and event origination time. The results of the analysis are distributed to States Parties and other users by various means.

Figure 1 shows the logical organization of the IDC software. The Automatic Processing computer software configuration item (CSCI) runs unattended and is the first step in the data interpretation sequence. The modules in this CSCI are configured to form processing pipelines.

The Radionuclide Automatic Processing includes the following five computer software components (CSCs):

- Radionuclide Detection Processing

  This CSC consolidates data for a given sample and performs an automated analysis to identify and quantify the radionuclides that are present. Results are stored in the RMS database. Software for this CSC is used for both automated processing and interactive review.

- Radionuclide Characterization Processing

  Software for this CSC is used for both automated processing and interactive review. The automated reults of this CSC are nuclide and sample prioritization levels while the interactive results are nuclide and sample categorization levels. Levels are assigned according to the type of nuclides identified (natural vs. anthropogenic) and the activity concentration determined (normal vs. abnormal). Results are stored in the RMS database and alert messages may be sent to subscribers (for automated processing only).

- Radionuclide Processing Control

  This CSC executes whenever email is received by a user account specifically configured for that purpose. If the message contains pulse height data (PHD), the Radionuclide Processing Control CSC controls the execution of and data flow through the automated Radionuclide Detection and Characterization Processing.

- Radionuclide Import Processing

  This CSC parses and stores data in the database for all data messages sent through the pipeline. If the message contains a spectrum or a histogram, this CSC will store it to a file for later use.

- Radionuclide Export Processing

  The Radionuclide World Wide Web site permits access to radionuclide data products and provides general information regarding the Radionuclide Monitoring System (RMS).

The Radionuclide Interactive Processing Software includes the following six CSCs:

- Inspectra

  Inspectra is the primary review tool for the radionuclide analyst to view raw data and results of gamma-ray spectroscopy systems. Inspectra displays both the raw spectrum data and the processed spectrum data to the analyst. As part of the review process, an analyst can add comments, edit peaks, and unflag nuclide identifications. The analyst also has the ability to reanalyze a sample from scratch. When a spectrum review is finished, the raw spectrum data, processed spectrum data, and reviewed spectrum data are written to a Reviewed Radionuclide Report (RRR) file accessible via the Web.

- CORIANT

  The Coincident Radiation Interactive Analysis Tool (CORIANT) allows analysts to review 3-D beta-gamma coincidence data. As part of the review process, an analyst can add comments and reanalyze the sample. This GUI displays histograms, beta-gated gamma spectra, gamma-gated beta spectra, and analysis results.

- Multiple Analyst Review Tool

  The Multiple Analyst Review Tool allows a specified user to customize the automatic distributions of samples from automatic processing and to define the functions each user is permitted to execute while interactively reviewing a sample and interacting with the database.

- Trendvue

  Trendvue software provides an intuitive and robust graphical interface for visualizing radionuclide analysis and state-of-health data.

- Analyst Work Area

  The Analyst Work Area is an intranet tool that facilitates the ability to identify and prioritize spectral data that requires review upon its arrival at the IDC.

- Workflow

  The Workflow software is a graphical user interface (GUI) that displays receipt of data, the state of radionuclide blowers and detectors at stations and laboratories, and the collection of State of Health (SOH) data.

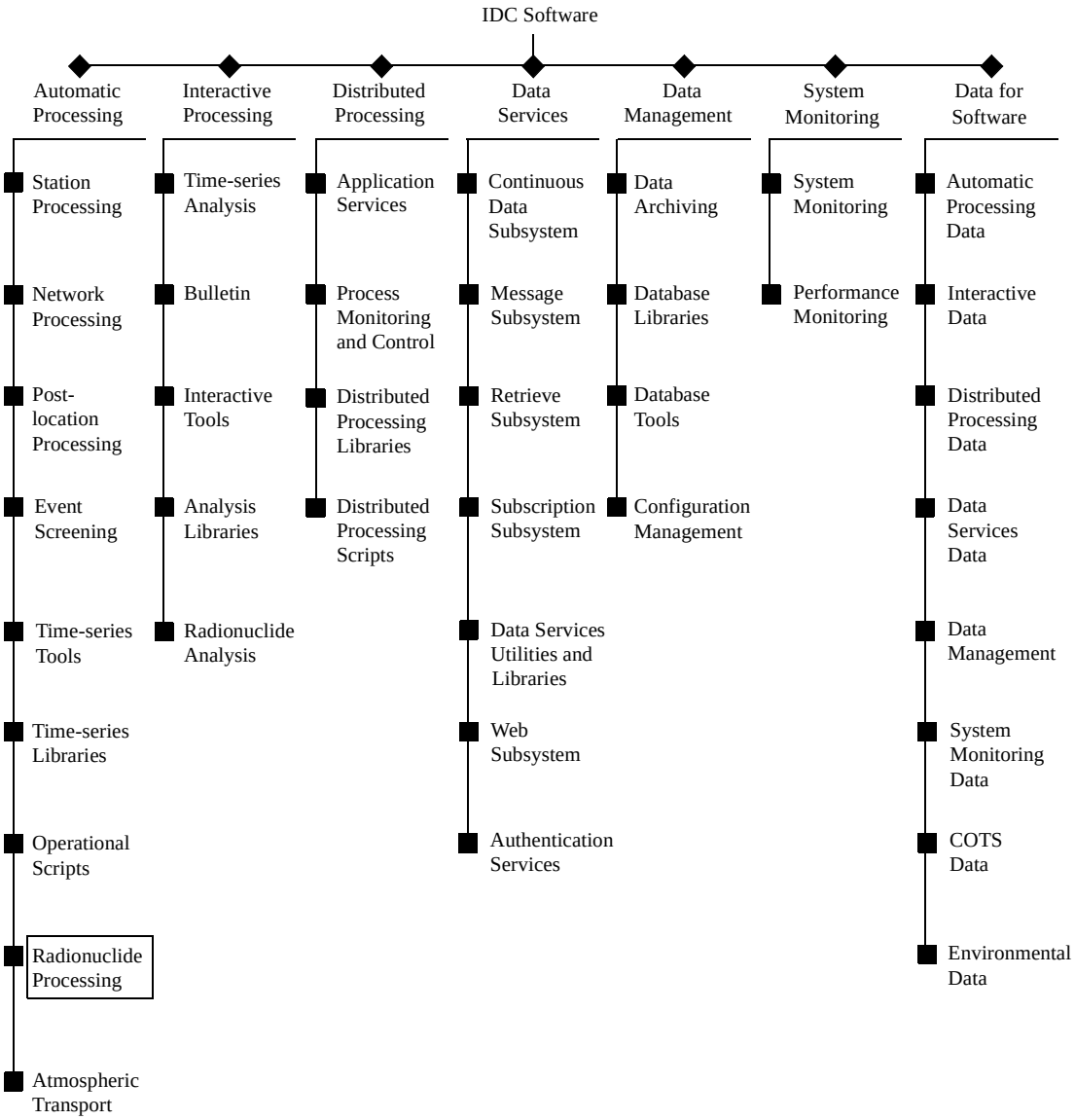


FIGURE 1. IDC SOFTWARE CONFIGURATION HIERARCHY

STATUS OF DEVELOPMENT

This is an upgrade to the third version of the radionuclide software to be formally released. It differs from earlier version releases in that it's primary focus is software bug resolution; however, it does in some cases provide enhancements and new functionality.

FUNCTIONALITY

Software Relationships

The IDC software acquires time series and radionuclide data from stations of the International Monitoring System and other locations. The relationship of software units of the automatic processing CSCIs is illustrated in Figure 2.

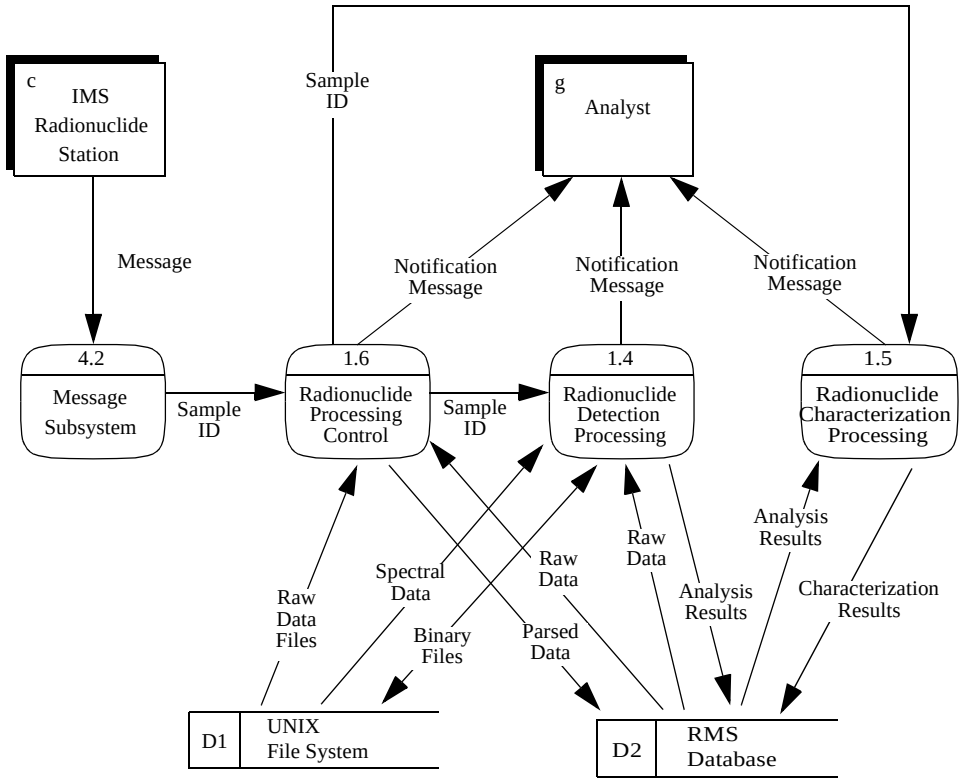


FIGURE 2. RELATIONSHIP OF SOFTWARE UNITS OF AUTOMATIC PROCESSING CSCIS

Equipment Familiarization

Interactive software application windows display screens that can be resized by using one of four resize corners or the maximize button. To enlarge a window, select one of the four resize corners and drag the corner to the desired screen size. A pointer designed as an arrow appears when the Inspectra software is accessed. Pointer movement occurs by moving the mouse. Selecting a textbox quickly changes the pointer to a cursor and functions via keyboard input. The arrow reappears with any mouse movement.

OPERATIONS

These applications are part of the RMS software installation and include both automated processing software and interactive radionuclide analysis tools. The automated processing software requires installation of the Canberra UNIX library software and licensure. All of the software components require access to an ORACLE relational database management system (RDBMS), Server version 8i, and ORACLE client software SQLNET 2.1. The RMS system requires the Solaris 2.7 operating system, X Windows Release 5, and Motif 1.22. (Subsequent versions of the operating system software are expected to be compatible with the RMS software.)

The RMS system requires three basic hardware elements, which can be run on the same machine or on different machines. The minimum hardware requirements are defined below:

- The ORACLE DBMS server should run on a SPARC20 with at least 96 megabytes (MB) of random access memory (RAM) and 1 gigabyte (GB) of hard disk space.
- The Automated Processing software requires a SPARC20 with a minimum of 96 MB of RAM and 1 GB of hard disk space.
- The Interactive Analysis Tools require a SPARC20 with a minimum of 96 MB of RAM.

Chapter 2: Basic Procedures

This chapter provides step-by-step instructions for using the radionuclide monitoring software.

Chapter 2: Basic Procedures

This chapter describes how to gain access to the software, how to use basic commands, and how to end a session.

INSTALLATION AND SETUP

This manual assumes that the radionuclide software is installed and running on your system.

Access Control

You must have a logon to the ORACLE database with permission to view the radionuclide database tables. No other password is required to access this software.

Passwords

A password is a sequence of characters and/or integers used in the logon procedure to gain admittance to the RMS database. To obtain or change your password, contact your System Administrator.

GETTING STARTED

Instructions on starting each software component are included in the respective chapters.

USING MENUS

To use the menubar, click the desired menu. A pull-down menu appears. Drag and select the desired function.

USING COMMON COMMANDS

An underscore below a letter on the menubar or a pull-down menu selection indicates a short-cut key. Pressing the underscored letter activates that particular function.

OBTAINING HELP

For help in using the Radionuclide software, refer to the step-by-step instructions in each chapter.

STOPPING/SUSPENDING WORK

To stop or suspend your work proceed as follows:

1. To suspend work, click the minimize button on the application window.

   A small icon appears in the lower, left-hand corner of your screen.

2. To return to the Inspectra application, double-click the minimized application icon.

   The application reappears.

3. To exit the application from the application window, choose File>Exit.

   You are returned to the UNIX prompt.

Chapter 3: Inspectra Procedures

This chapter provides step-by-step instructions for using the Inspectra Radionuclide software and includes the following sections:

- Overview
- Feature-specific Procedures
- Illustrative Interactive Analysis: Particulate Sample
- Customizing Software

Chapter 3: Inspectra Procedures

OVERVIEW

The purpose of the radionuclide interactive processing system is to provide organized, relevant data in a format that can be used by analysts, scientists, processing engineers, and technical management for radionuclide monitoring. The Inspectra software is a graphical user interface (GUI) that facilitates review of automated high-resolution gamma-ray spectroscopy results and related spectral data.

FEATURE-SPECIFIC PROCEDURES

This section provides detailed instructions for using the software's features. These procedures also identify and describe the Inspectra main application window menu selections and special dialogs.

Getting Started

To start Inspectra, proceed as follows:

1. At the UNIX prompt, type `rms_inspectra` and press the Return key.
   The Database Connection Dialog appears, Figure 3.

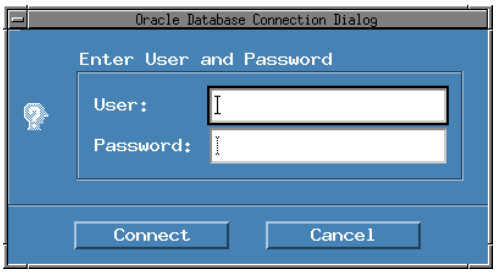


FIGURE 3. ORACLE DATABASE CONNECTION DIALOG

2. Enter information appropriate to your system.
   - Activate each text box by pointing and clicking.
   - After information is entered, click Connect.
3. If incorrect data are entered, a message Error appears, `"ORA-01017: invalid username/password; login denied."` Click Cancel. As in all cases, the Oracle command line utility "oerr ora error #" provides a text description of Oracle generate errors. For example, at the command line type "oerr ora 1017" and the error text noted above is returned.
4. The ORACLE Database Connection Dialog reappears. After correct data are entered, click Connect.

   With proper login, the Inspectra Tool window appears.

Spectrum Menu Selections

The selections available in the Spectrum menu are shown in Table 1; each selection is discussed in turn.

TABLE 1: SPECTRUM MENU SELECTION

Selections	Function
Database Connect	Connects to various databases (active at the PIDC only).
Open Sample	Displays a spectrum.
Open Sample ID	Opens sample using sample identification (SID) number.
Reload Sample	Updates sample information from database to Inspectra.
Close Sample	Closes open sample(s).
Sample Assignment Queue	Displays a list of samples assigned to each user (MAR interface).
View General Comments	Displays analyst comments that appear within spectrum heading.
View Station Comments	Displays station operator comments.
Print RRR	Prints Reviewed Radionuclide Report (RRR).
Exit	Exits application.

Database Connect

Database Connect takes place during the login procedure and becomes inactive, or grayed out, once you have successfully connected to the database.

Open Sample

The Open Sample selection provides the ability to query the RMS database for a spectrum or group of spectra according to particular specifications. For example, you can query the database for spectra from a particular detector and/or for a specific month. The results of a query appear in the table. From these query results, a spectrum can be displayed graphically.

User Requirements

When performing a query or requesting the display of a spectrum, please note the following requirements.

1. The Tab key must be used to move among the data fields in which data are manually entered. If this is not done, the query displays the following response, "`No records were found`." This message may also appear if a user enters a query for which there is no data, for example, a future date.
2. To enter data, click the button below each heading and drag to the desired selection on the pull-down menu. If there is not a button beneath the heading, press the Tab key or click the column in the first row of the table and key in the appropriate data. Be sure to use the Tab key to move out of fields where data are manually entered. (Please note, each column does not require data to execute a successful query.)
3. The percent symbol (%) acts as a wildcard replacing characters that would normally be entered manually. In the following illustrative procedure, the % is entered in the C Stop column (for example, `1997-01-%`), which specifies a query for all spectra during the first month of 1997. (If a request such as `%-01-%` is entered in the C Stop column, all data from the first month of all years for which there are data in the database would be listed, but only up to 150 records.)
4. A query requires a date be set in the format YYYY-MM-DD hh:mm:ss to specify year, month, day, hours, minutes, and seconds. The wildcard, %, can be used anywhere in such a data input string.
5. The query provides the message, "`No records found`," if none are located following the execution of the query. If this happens, click Reset Query and enter new data to execute another query.

The Open Sample Dialog does not disappear when Apply is chosen as it does when OK is selected; the dialog remains in the foreground even after the selected spectrum is displayed.

To open a sample, proceed as follows.

1. Choose Spectrum>Open Sample.

   The Open Sample Dialog appears.

   In some cases, a column can contain more information than what is first displayed with the current grid size. These columns display a small arrowhead to the right of the information.

   – To display additional data, change the grid size by moving the pointer to touch one of the grid lines.
     An arrow with a short line segment appears.
   – Click and drag the grid line to the right to enlarge (or to the left to reduce) the size of the column viewing area.
     The small arrowheads disappear when all data are displayed.

2. Click Station and select a station from the pull-down menu.
3. Click Detector and select a detector from the pull-down menu.
4. Press the Tab key to advance to the C Stop column and enter a date, if needed, for the desired query.
5. Press the Tab key to exit the C Stop column.
6. Press the Tab key to advance to the Acq Start column and enter a date, if needed, for desired query.
7. Press the Tab key to exit Acq Start column.
8. Click Status and select a sample status from the pull-down menu.
9. Click Qual and choose a spectral data qualifier from the pull-down menu.
10. Click Data Type and choose the type of acquisition count from the pull-down menu.
11. Click Sample type and choose the type of sample from the pull-down menu.
12. Click Execute Query.

    A table listing all spectra that fit your query are displayed. The first line contains your actual query.

13. Select the line containing a spectrum to be displayed.

14. Click OK.

    Before the selected spectrum appears in the Inspectra Tool Window, an Inspectra Message box may appear indicating that the chosen sample is not currently assigned and that opening this sample will be READ ONLY. Once a spectrum is displayed, you may want to view additional samples. To open additional samples, repeat steps 1-10. As many as ten spectra can be opened at a time, but only one spectrum will be displayed.[1] See the discussion on "Spectrum Characteristics" on page 37 for features and characteristics of the spectrum graph.

15. To begin a new query and clear entries from the query line, click Reset Query and follow steps 1-10.

Data Field Attributes in the Open Sample Dialog

Each of the field headings in the Open Sample selection are interactive. That is, field headings provide multiple options that allow you to set a query as narrow or as broad as necessary. The following field headings appear at the top of the Open Sample Dialog and are discussed below: Station, Detector, C Stop (Collection Stop), Acq Start (Acquisition Start), Status, Qual (Qualifier), Data Type, Sample Type, and SID.

- Station - A pull-down menu provides a listing of all stations in the RMS database, as well as a Clear option where no specific station is chosen.
- Detector - A pull-down menu provides a listing of all detectors in the RMS database, as well as a Clear option where no specific station is chosen.
- C Stop - This field permits the retrieval of spectral data associated with a given collection stop. Entering a year, month, and day in this field sets a very specific query. The results of this query are displayed in descending order.

1. It is possible to open more than one Inspectra on a single monitor, however the screen space available for each spectrum is reduced. Two monitors can be used to display spectra side-by-side, if the computer system is configured to permit Inspectra to be opened on both monitors.

- Acq Start - This field permits you to set a query based on spectral data associated with the Acquisition Start. Once again, entering a year, month, and day sets a very specific query. Query results are displayed in descending order.
- Status - This field permits you to display spectra at various points in the spectral analysis process. Each query choice is discussed in turn.
  - Clear - No criteria are set.
  - Reviewed - An interactive review of the spectrum has been completed and the results have been released to the export process. (In the case of the PIDC, data are released to the Web.)
  - Unprocessed - The spectral data set has not proceeded through the automatic analysis process, *rms_analyze*.
  - Analysis - The spectral data set did not successfully proceed through *rms_analyze*, possibly because of incorrect input.
  - Processed - The spectral data set successfully proceeded through *rms_analyze*.
  - Viewed - An analyst has viewed the spectrum, but did not complete the interactive analysis.
  - Bad Calibration - A given detector has experienced calibration problems.
  - Hold for Review - An analyst released a spectrum to another user identity.
- Qual - This is a qualifier for spectral data depending on the acquisition duration. The following choices are available: Clear, FULL, or PREL (Preliminary).
  - Clear - This choice does not set criteria.
  - FULL - This selection requests only samples that have been counted for the full acquisition duration.
  - PREL - This selection requests only samples that have been counted for less than the full acquisition duration.
- Data Type - This refers to the type of acquisition count: Clear, Blank, Calibration, Det. Background, Quality Control, and Sample.
  - Clear - No criteria are set.

  - Blank - This choice requests spectral data from an unexposed filter (not relevant for noble gas samples).
  - Calibration - This spectral data type represents a count of (usually a certified) radionuclide source used in the calibration of a given detector.
  - Det. Background - This choice requests spectral data from an acquisition of an empty detector chamber.
  - Quality Control - Displaying this spectral data set permits you to determine if a detector is operating within an acceptable range or if recalibration of the detector is in order. Such spectral data types are commonly acquired between sample counts using a certified multi-nuclide source.
  - Sample - This is a standard detector acquisition.

- Sample Type - This refers to the type of sample to be analyzed. The choices are Clear, Gas, and Particulate. Note that Inspectra is not designed for the review of beta-gamma coincidence data. Therefore, the sample type "B" has been filtered out from all Open Sample Dialog options in Inspectra
  - Clear -No criteria are set; both gas and particulate data are displayed.
  - Gas - This option will display only noble gas samples.
  - Particulate - This option will display only particulate samples.
- SID - This refers to a specific sample identification.

Open Sample Exercise

To query the RMS database for a group of spectra, proceed as follows:

1. Choose Spectrum>Open Sample.
2. Choose Station>KW001.
3. Choose Detector>KW001KWB1.
4. Choose Status>Reviewed.
5. Choose Qual>FULL.
6. Choose Data Type>Sample.
7. Choose Sample Type>Particulate.

8. Click Execute Query.

   The data appearing in the Open Sample Dialog shown in Figure 4 are the query response. It should be noted that records from the period specified are shown in descending chronological order. A query can display as many as 150 records at a given time.

9. Select the row containing SID 20133 and click OK. (Do not choose the first row as it displays the query parameters). Please note that this spectrum may have READ ONLY permissions.

   The selected spectrum appears in Inspectra's Main Window (Figure 5).

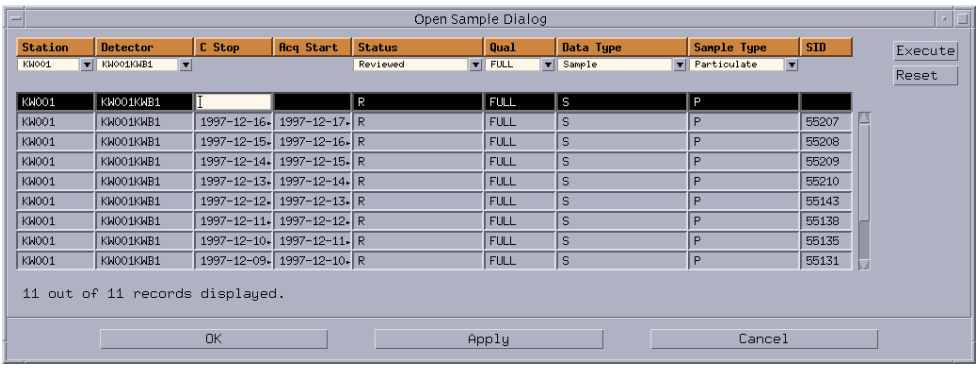


FIGURE 4. ILLUSTRATIVE PROCEDURE QUERY RESULTS

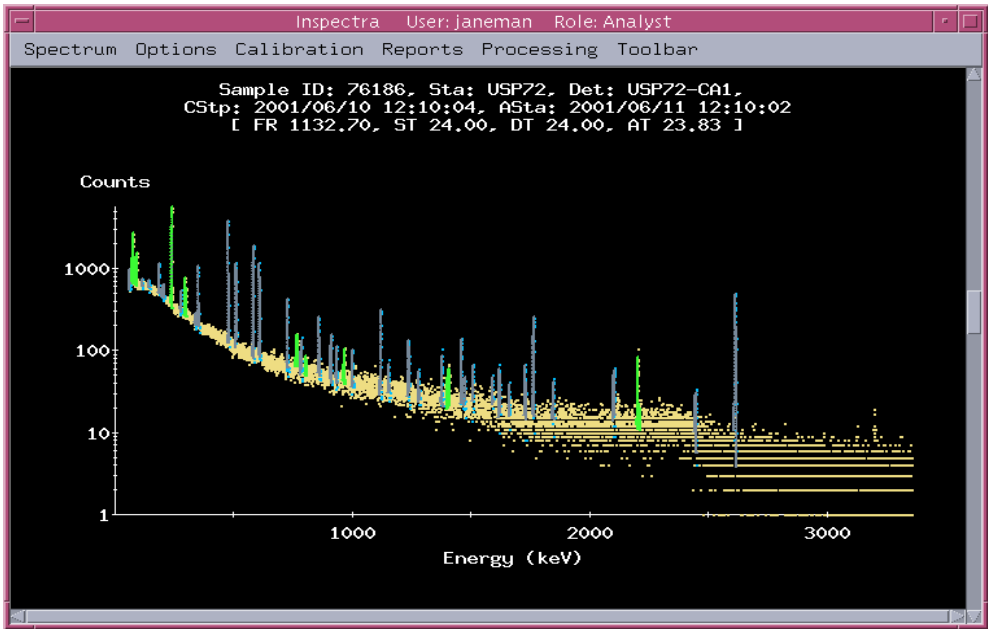


FIGURE 5. GRAPHICAL DISPLAY OF A SPECTRUM IN INSPECTRA'S MAIN WINDOW

Spectrum Characteristics

After selecting a spectrum, using one of the Open Sample, Open Sample ID (with potential READ ONLY permission) or Sample Assignment Queue options, the Inspectra Tool's main window displays a graph having various characteristics and features. For ease of use, the user's login name and the current role have been added to the title bar on the main window of Inspectra. NOTE: Other Figures in this document which depict the main Inspectra window may not display this updated title bar. An effort was made to keep the original Figures appearing in the R3 documentation, where possible, in order to preserve their content .

- Characteristics of the Spectrum Graph

  The Inspectra Tool window selections (Spectrum, Options, Calibration, Reports, Processing and Toolbar) appear with the spectrum.

  The specifications pertaining to the spectrum are displayed using the following abbreviations:

  - Sample ID - sample identification (same as SID)
  - Sta - station
  - Det - detector
  - CStp - collection stop (UTC)
  - ASta - acquisition start (UTC)
  - FR - flow rate (average, in cubic meters per hour)
  - ST - sampling time in hours
  - DT - decay time in hours
  - AT - acquisition time in hours

- Energy is shown on the x-axis in Kiloelectron Volts (keV). The relationship between energy and channels depends on how individual detectors are set up. To see the equation that defines this relationship, see "Equations" on page 60.
- Data on the graph may be color-coded to highlight important aspects of a spectrum. Various aspects of a spectrum, including color coding, are configurable and described in "Configuration" on page 46.
- Clicking anywhere on the sample spectrum graph activates a solid vertical line. This line marks specific points on the graph and displays the corresponding Channel, Energy, and Count values below the spectrum along the horizontal axis.

Expand Feature

A spectrum can be enhanced by expanding or zooming in on a specific region. To use the expand feature, proceed as follows:

1. Without pressing any mouse buttons, position the pointer next to an area of interest on the graph (such as to the right or left of a peak).

2. Pressing the Control key and the left mouse button simultaneously, move the mouse to the left or right. This action highlights the region of the spectrum to be expanded.
3. Release the mouse button and then release the Control key.

   The resulting highlighted area is enlarged as shown in Figure 6.

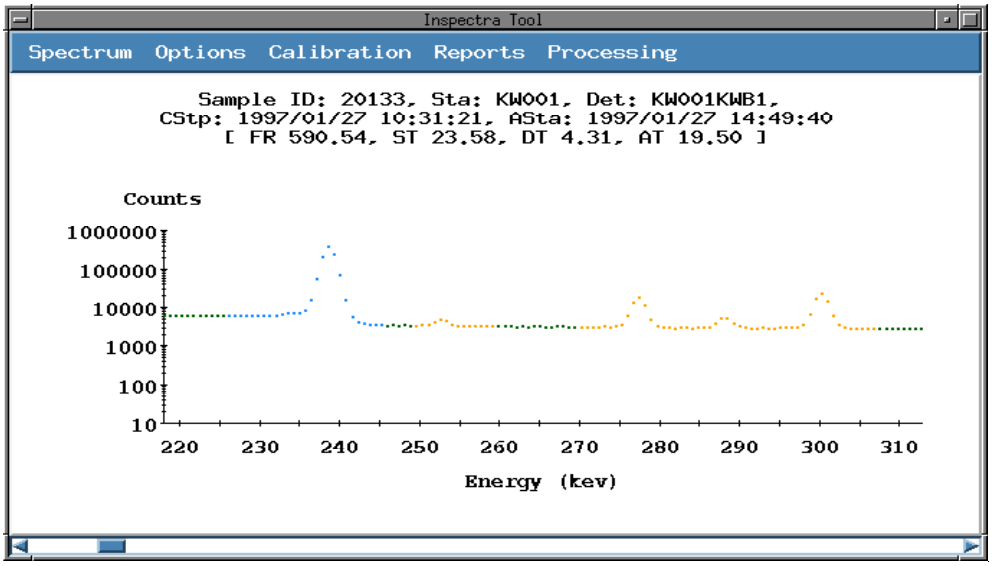


FIGURE 6. EXPANDED DISPLAY OF A SPECTRUM

4. Press the “a” key to scale the graph to screen size. Press the “r” key to return the spectrum to its original size unless reconfigured to user specifications. See “Plot Action Translations (Short-cut keys)” on page 50.
5. This procedure can be repeated as many times as necessary to expand any portion of the displayed graph.

Nuclide Identification Feature

Pressing and holding the middle mouse button at a data point displays all nuclides whose nuclide library energy matches the energy of that data point within some preset energy tolerance as shown in Figure 7.

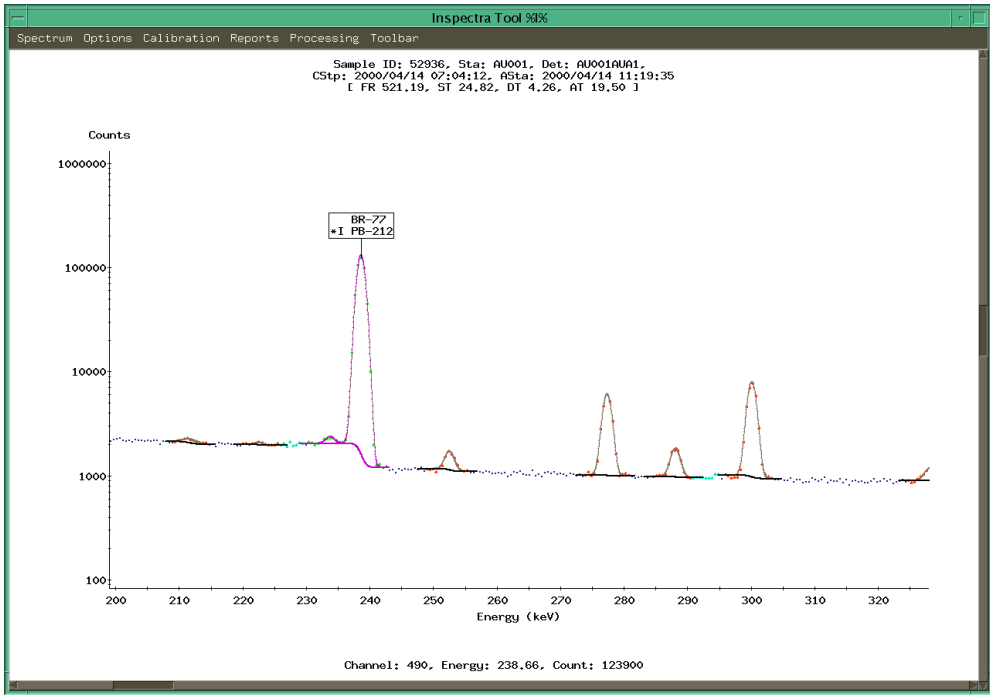


FIGURE 7. EXPANDED SPECTRUM IDENTIFYING NUCLIDES AT A GIVEN DATA POINT

In the above example, according to the nuclide library, ^{212}Pb and ^{77}Br are possible candidates for the nuclide associated with the energy of this data point.

- The "I" indicates that ^{212}Pb was associated with one or more lines in the peak search report; however, it does not necessarily mean that it is associated with this particular peak. In this example, this peak does indeed correspond to the keyline for ^{212}Pb at 238.55 keV.

- An asterisk (*) indicates that this energy corresponds to the nuclide's keyline as defined in the nuclide library.
- The flag "None" appears if the energy of that particular data point is not associated with a nuclide in the library.

Pressing the Control key and the middle mouse button simultaneously in the above example will display only those nuclides whose keyline is at that energy region of the spectrum, namely ^{212}Pb.

Scroll Feature

Once the expanded spectrum graph is displayed, a scroll bar extends along the bottom edge of the dialog. The horizontal scroll bar is used to move to the left or right of an expanded spectrum.

Enhancing the Spectrum Graph

A spectrum graph can be enhanced using short-cut keys and selecting various spectrum plot settings, see "Options Menu Selection" on page 46.

Opening Sample IDs

The Open Sample ID selection displays a spectrum by keying the SID number directly into the Open Sample ID Dialog text box. To open a sample using the SID, proceed as follows:

1. Choose Spectrum>Open Sample ID.

   The Open Sample ID Dialog appears.
2. Select the highlighted text box and type in the SID.

3. Click OK or Apply to display the spectrum. An Inspectra Message window will appear indicating the user to whom the spectrum has been assigned as well as the given permissions for the current user. The window remains open when selecting Apply and closes when selecting OK. This window lists all open samples.

   The spectrum appears in the Inspectra Tool window.

Reloading Samples

The Reload Samples selection provides the ability to confirm and review actions made to the RMS database. To reload a sample, proceed as follows:

1. Choose Spectrum>Reload Sample.

   The Reload Confirmation Dialog appears.

2. Select Yes or No to reload a sample. An Inspectra Message window will appear indicating to whom the spectrum is assigned as well as the given permissions for the current user.

   You are returned to the Inspectra Tool window.

Closing Samples

The Closing Samples selection provides the ability to close a single sample or multiple samples at a given time. To close a sample, proceed as follows:

1. Choose Spectrum>Close Sample.

   The Close Sample ID Dialog appears (Figure 8).

2. To close a single sample, select an SID.
3. Click Close.
4. To close more than one sample at a time, click and drag the mouse over several SIDs.

   Several SIDs are highlighted.

5. Click Close.

   The Close Sample ID Dialog is closed. When Apply is clicked, the selected samples close, but the Close Sample ID Dialog remains open.

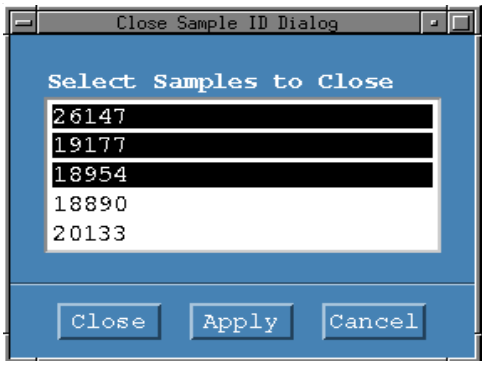


FIGURE 8. CLOSE SAMPLE DIALOG

Sample Assignment Queue

The Sample Assignment Queue is a pop-up window that displays radionuclide samples and the roles and users to whom they have been assigned. Roles are assigned to users via the Multiple Analyst Review (MAR) Tool. (For more information on how roles are assigned, see “MAR Tool Procedures” on page 119.) The Sample Assignment Queue displays the samples currently awaiting review, plus some related sample data. This should be considered the "inbox" for an analyst using Inspectra.

To access the Sample Assignment Queue, proceed as follows:

1. Choose Spectrum>Sample Assignment Queue.

   The Sample Assignment Queue Window appears. The table will be loaded with the samples assigned to your default role.

2. If you do not have a default role assigned, then the Select Identity box in the lower right corner will be empty and the Sample Assignment Queue will be blank. To choose a role, click the button beside Select Identity and highlight the desired role. The table will be loaded with samples assigned to this role.

Samples that have been assigned to the current role in the Select Identity box have WRITE status, meaning you are able to make changes and update database tables. The Select Identity box lists all the roles assigned to the current user.

When a role is selected, Inspectra checks for permission authorization, noting what functions the selected role is permitted to execute while reviewing a sample. If you have been assigned more than one role, you may change roles in the Select Identity box in order to have WRITE permission on samples assigned to your other roles. For example, after accessing samples assigned to Analyst, the user may select Lead Analyst in the Select Identity box to access a different set of samples with WRITE permission.

When reviewing samples with Inspectra, an analyst's first priority should be to verify that the correct role is selected in the Select Identity box. If no role is selected in the Select Identity box, then all samples viewed will be READ ONLY, limiting access and functionality.

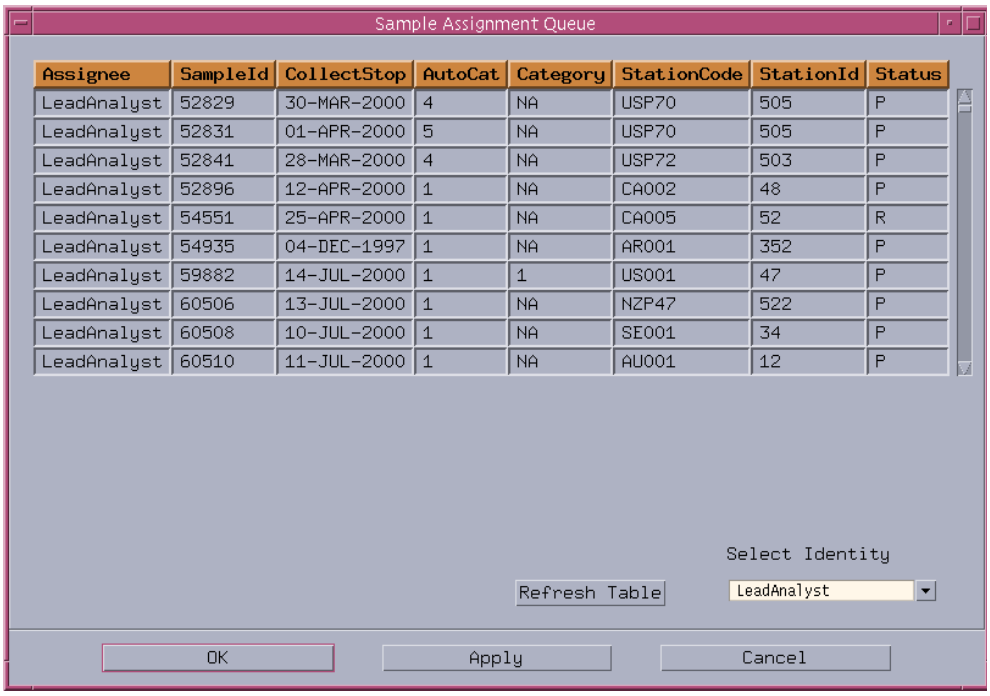


FIGURE 9. SAMPLE ASSIGNMENT QUEUE WINDOW

Viewing General Comments

This selection provides the ability to view analyst's comments on a given sample once the sample is opened.

To access this selection a sample must be opened. Proceed as follows:

1. Choose Spectrum>View General Sample Comments.

   The View General Sample Comments dialog appears.

2. Click Cancel.

   You are returned to the Inspectra Tool window.

Viewing Station Comments

This menu selection opens the Sample Station Comments Dialog, which provides a station operator's comments. To access this selection a sample must be open. Instructions are as follows:

1. Choose Spectrum>View Station Comments.

   The View Station Comments Dialog appears.

2. Click Cancel.

   You are returned to the Inspectra Tool window.

Print RRR

This selection prints a Reviewed Radionuclide Report (RRR).

To access this selection, proceed as follows:

1. Choose Spectrum>Print RRR.

   The Print RRR Confirmation Dialog appears.

2. Click Print.

   You are returned to the Inspectra Tool window.

Options Menu Selection

The Options menu provides the capability to configure the Inspectra Tool for spectrum analysis. Table 2 provides an overview of the Options menu selections and their functions. Each option is discussed in detail below.

TABLE 2: OPTIONS MENU SELECTIONS

Selections	Function
Configuration	Configures plots, data styles, and plot action translations.
ROI	Allows the analyst to add missed peaks, remove false peaks, and modify poorly defined peaks.
Compare Dialog	Allows the analyst to view two spectra simultaneously.
Nuclide Review	Displays the spectral data points that surround the four most abundant lines of the selected nuclide.
Residual Plot	Displays the residual plot
Peak Sig/PSS	Displays the peak search sensitivity and peak significance scatter plot.

Configuration

The Configuration selection provides a dialog with three tabs: Spectrum Plots, Spectrum Data Styles, and Plot Action Translations. Each configuration tab is discussed below.

To implement configuration changes, proceed as follows.

1. Choose Options>Configuration.

   The Configuration Dialog appears. The Configuration Dialog uses generic buttons for each selection. When selecting the Show Global Resources check box, all changes are automatically implemented globally and saved to the file `$HOME/.inspectra.rc`. This file should never be edited. If any changes are manually made to this file, they are made at the user's own risk. Clearing the Show Global Resources option ensures that changes only affect the spectrum currently displayed.

2. Click the Tab to perform the desired reconfiguration. (Each tab is discussed below.)
3. Select options to activate desired functions.
4. When entering changes in a text box, select the appropriate text box in the matrix, enter the change, and use the Tab key to exit the text box.
5. To implement or cancel your configuration options, choose one of the following:
   - Click OK to implement changes and close the Configuration Dialog box.
   - Click Apply to implement changes and maintain an open Configuration Dialog.
   - Click Cancel to close the dialog without implementing any changes.

   After one of the above selections, you are returned to the Inspectra Tool window.

Spectrum Plots

The Spectrum Plots tab can configure the data displayed on a spectrum plot, thereby enhancing the analysis of a given spectrum. The function of each configurable plot setting is described in Table 3. (Color settings of data are discussed in "Spectrum Data Styles" on page 48.)

TABLE 3: SPECTRUM PLOT SETTINGS AND FUNCTIONS

Setting	Function
Singlets	Hide/display single peaks (singlets).
Multiplets	Hide/display multiple peaks (multiplets).
Indicated Blank Subtr ROIs	Hide/display blank subtraction of a region of interest (ROI).
Nuclides of Interest	Hide/display color-coded radionuclide fission products as defined in [WG195][1].

TABLE 3: SPECTRUM PLOT SETTINGS AND FUNCTIONS (CONTINUED)

Setting	Function
Peak Fit: Baseline	Hide/display step function for the baseline in an ROI.
Peak Fit: Initial	Hide/display initial peak fit in an ROI prior to blank subtraction.
Components	Hide/display individual peaks in a multiplet.

1. The WP-224 nuclides of interest are for particle analysis requirements: ^{95}Zr, ^{95}Nb, ^{97}Zr, ^{99}Mo / ^{99m}Tc, ^{103}Ru, ^{131}I, ^{132}Te, ^{133}I, ^{134}Cs, ^{136}Cs, ^{137}Cs, ^{140}Ba, and ^{143}Ce. For noble gas analysis requirements: ^{131m}Xe, ^{133}Xe, ^{133m}Xe, and ^{135}Xe.

The following describes the above settings in greater detail.

- Singlets and Multiplets - When these selections are checked, single and multiple peaks are highlighted in the spectrum with different colors.
- Indicated Blank Subtraction of ROI - This selection is available, but not in use at this time (see "Peak Search" on page 64).
- Nuclides of Interest - When this selection is checked, anthropogenic radionuclides associated with nuclear explosive devices are highlighted in the spectrum display.
- Peak Fit Baseline and Peak Fit Initial - When these selections are checked in the spectrum display, the fitted peak and baseline are highlighted with different colors, as configured in the Spectrum Data Styles tab, Figure 10. The peak fits are performed by the automatic analysis routines, and when displayed provide the reviewer a tool to measure how well the calculated functions fit the actual data.
- Components - It hides or displays the peaks in a mulitplet

Spectrum Data Styles

The Spectrum Data Styles tab allows the user to configure colors, line width, and point size of various spectrum features (Figure 10).

Specific to this tab are the Show X Marker, Show Y Marker, and Area Graph settings. Selecting the Show X Marker check box provides a vertical pointer, selecting the Show Y Marker check box provides a horizontal pointer, and selecting both check boxes provides a cross-hair pointer (Figure 11). Area Graph converts the spectrum to a color blocked graphical display, allowing for enhanced ROI representation.

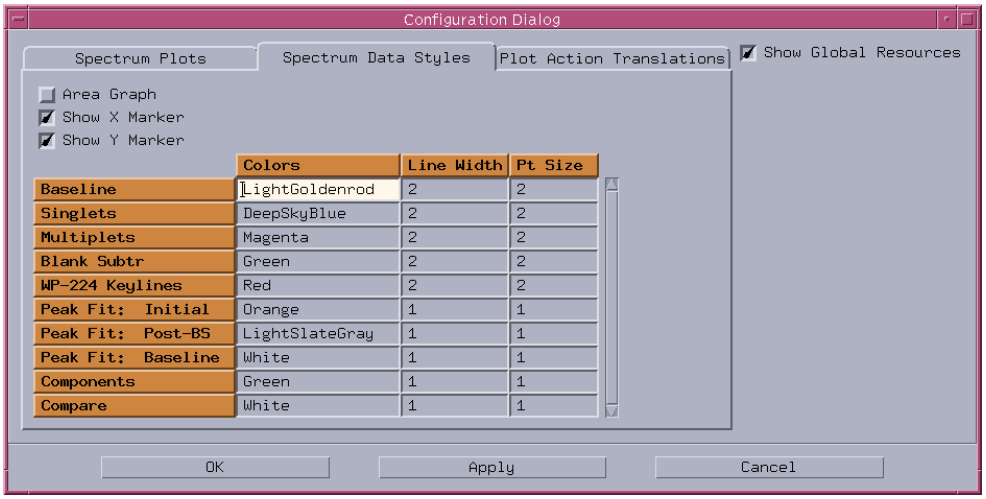


FIGURE 10. CONFIGURABLE SPECTRUM DATA STYLES

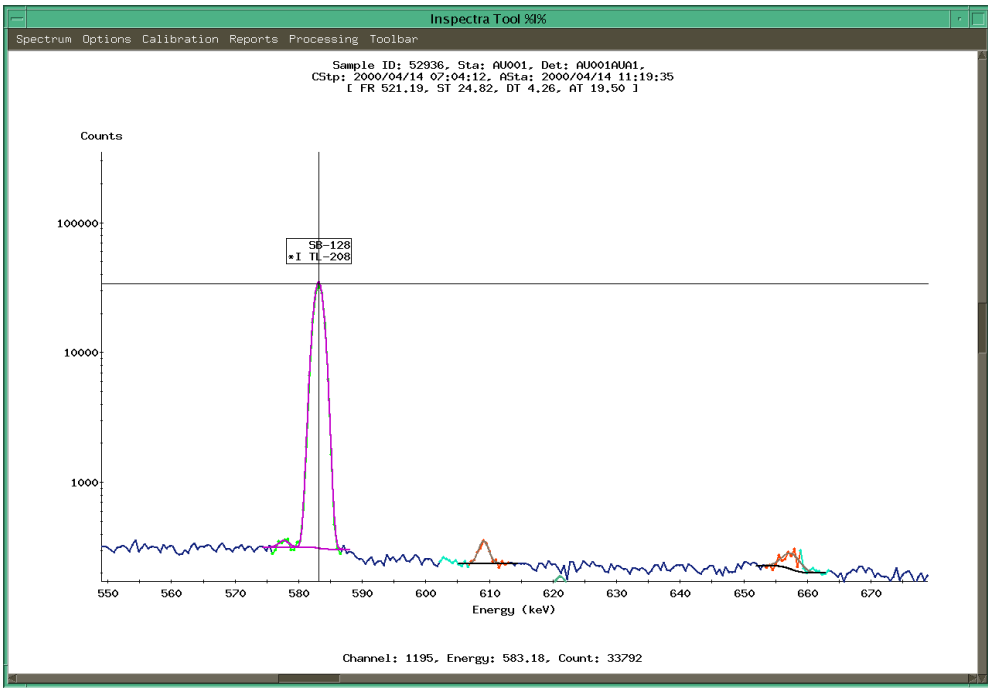


FIGURE 11. SPECTRUM EMPLOYING X-Y MARKER AND NUCLIDE IDENTIFICATION FEATURE

Plot Action Translations (Short-cut keys)

The Plot Action Translations tab allows the user to reconfigure spectrum enhancement settings. See Figure 12. The first column indicates an aspect of the plot that is configurable. The Ctrl and Shift check boxes select or clear the use of this key to perform specific functions. Clicking arrows on either side of the Media column switches between the Mouse and the Keyboard, indicating the device used to perform specific activities. Letters in the “Char” column correlate with the “Keyboard” in the Media column. Numbers in the “Char” column correlate with the “Mouse” in the Media column: 1= left mouse button, 2= middle mouse button, and 3= right mouse button. When entering data in a text box, rather than using the toggle button, type the change and use the Tab key to exit the text box.

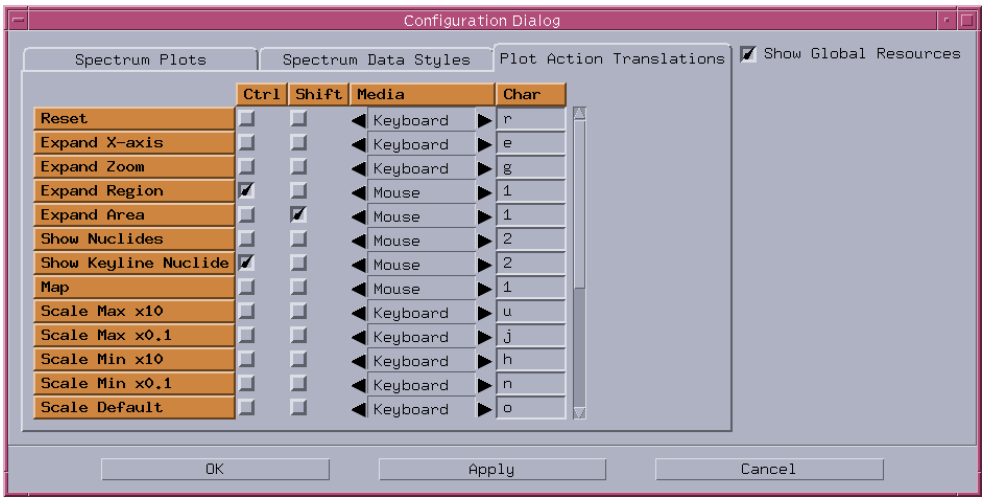


FIGURE 12. PLOT ACTION TRANSLATIONS

Each configurable aspect of the plot is described in Table 4.

TABLE 4: PLOT ACTION TRANSLATION FUNCTIONS

Plot Action	Function
Reset	Resets the spectrum to the original plot.
Expand X-axis	Expands the x-axis of a spectrum.
Expand Zoom	Expands the current zoom area.
Expand Region	Expands the highlighted ROI.
Expand Area	Expands the highlighted area of a spectrum (box format).
Show Nuclides	Displays nuclides whose library energy, ± some preset energy range, matches the energy of that data point.
Show Keyline Nuclide	Shows the keyline nuclide of a data point.
Map	Pointer control to locate a specific channel in a spectrum.
Scale Max x10	Expands the upper bounds of y-axis by 10x.
Scale Max x0.1	Decreases the upper bounds of y-axis by 0.1x.

TABLE 4: PLOT ACTION TRANSLATION FUNCTIONS (CONTINUED)

Plot Action	Function
Scale Min x10	Expands the lower bounds of y-axis by 10x.
Scale Min x0.1	Decreases the lower bounds of y-axis by 0.1x.
Scale Default	Returns the spectrum y-axis to the original scaling.
Scale Linear	Toggles between linear and logarithmic scale.
Scale Auto	Automatically scales the current plot view.
Plot Full	Toggles between full (all dots) and envelope (dots connected with lines) plots.
Move Left	Moves the pointer channel by channel to the left.
Move Right	Moves the pointer channel by channel to the right.
Compare Up	Shifts a comparison spectra up.
Compare Down	Shifts a comparison spectra down.
Resid Popup	Displays the peak fit and residuals for a selected peak.
Undo	Reverts spectrum display to its previous setting.

Region of Interest (ROI)

The Region of Interest dialog provides a method for adding missed peaks and modifying poorly defined peaks that are a result of the automated analysis processing. Please note that the results of the original analysis are always stored and all modifications are recorded.

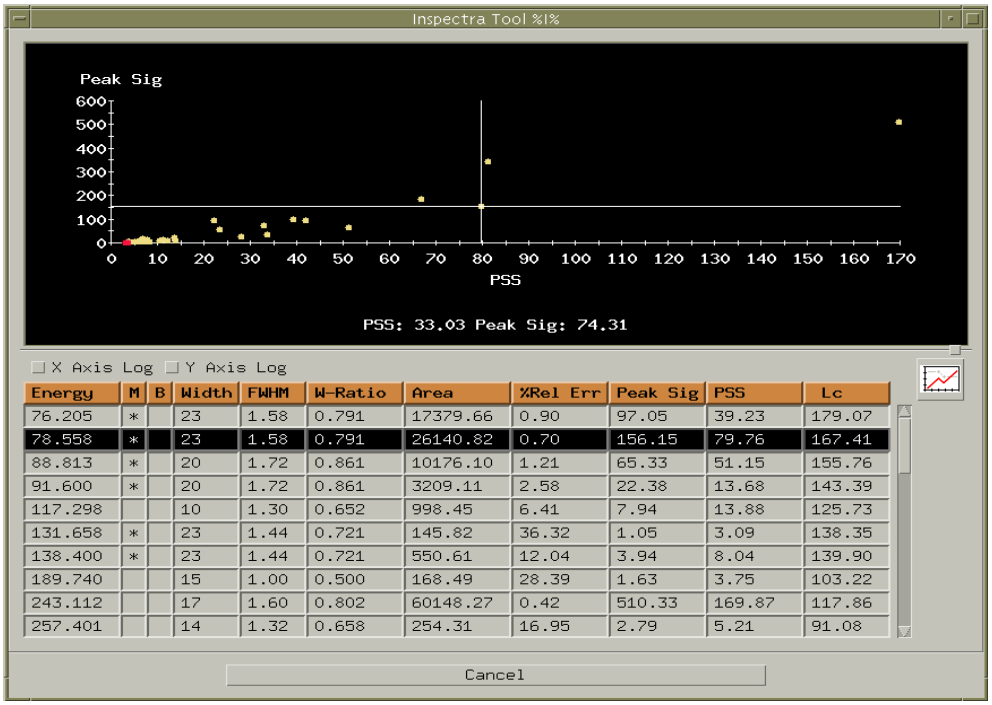
To use the ROI Tool, proceed as follows.

1. Choose Options>ROI.

   The Region of Interest Dialog appears (Figure 13).

2. Click Cancel.

   You are returned to the Inspectra Tool window.



Energy	M	B	Width	FWHM	W-Ratio	Area	%Rel Err	Peak Sig	PSS	Lc
76.205	*		23	1.58	0.791	17379.66	0.90	97.05	39.23	179.07
78.558	*		23	1.58	0.791	26140.82	0.70	156.15	79.76	167.41
88.813	*		20	1.72	0.861	10176.10	1.21	65.33	51.15	155.76
91.600	*		20	1.72	0.861	3209.11	2.58	22.38	13.68	143.39
117.298			10	1.30	0.652	998.45	6.41	7.94	13.88	125.73
131.658	*		23	1.44	0.721	145.82	36.32	1.05	3.09	138.35
138.400	*		23	1.44	0.721	550.61	12.04	3.94	8.04	139.90
189.740			15	1.00	0.500	168.49	28.39	1.63	3.75	103.22
243.112			17	1.60	0.802	60148.27	0.42	510.33	169.87	117.86
257.401			14	1.32	0.658	254.31	16.95	2.79	5.21	91.08

FIGURE 13. REGION OF INTEREST DIALOG

The ROI feature provides the ability to interactively test hypotheses for adding and modifying peaks. A new feature of this window for the Release 3 upgrade is the addition of cross-hairs to the graph. This allows for greater simplicity in reading the channels associated with a particular energy. The selected spectral region is displayed at the top of the dialog with the associated residuals directly below. The analysis results are displayed at the bottom of the dialog. When you click Apply or OK, changes are made and permanently recorded in the database.

The full spectrum is displayed with none of the original ROI results visible. This enables the user to clearly define a given ROI, regardless of the automatic analysis process results. Each ROI insertion must be treated as an independent action, and each ROI must be saved to disk before inserting another.

The ROI Dialog includes the expand features, x-y scale features, nuclide identification features, and marking data point features (each discussed earlier under their own heading) to provide added capabilities to the automated analysis process.

Adding a Peak Fit

To add a peak fit, proceed as follows.

1. Click the Left button, then select the left channel number of the given ROI you wish to insert.
2. Click the Right button, then select the right channel number of the given ROI.
3. Click the Add button, then select the centroid of the peak if the ROI is a singlet. If the given ROI is a multiplet, you must insert each peak centroid to the ROI by clicking the Add button multiple times. If you decide to remove one of the peak centroids you just added, click the Remove button. The FWHM++ and FWHM-- buttons (Full Width at Half-Maximum) are used to manually adjust the automatic peak fit(s) assigned to each peak centroid.
4. Click the Calculate button.

   Peak fit results are displayed in the ROI table with the associated residuals. The Diffs button will result in the display of a new Dialog window, which will indicate all the differences between the ROI actions just initiated, and those from the automatic analysis process.
5. You must choose to accept or reject the effects of adding a new peak.
   - Press the Cancel button to reject the new peak and exit the dialog.
   - Click Apply to accept the new peak and the results of the new identification.

     The results are stored in the database.
6. Click OK.

   You are returned to the Inspectra Tool window.

Modifying a Peak

To modify a peak, perform the same steps used in adding a peak fit.

Compare Dialog

The Compare dialog provides a method for viewing two peaks on the same graph. To use the compare tool, proceed as follows:

1. Choose Options>Compare Dialog.

   The Compare Dialog appears (Figure 14).

2. Click Cancel.

   You are returned to the Inspectra Tool window.

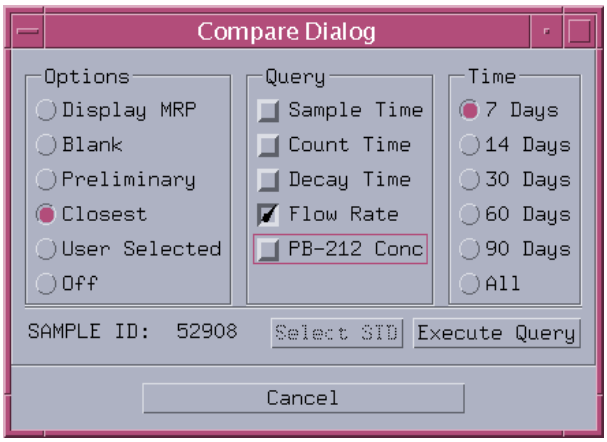


FIGURE 14. COMPARE DIALOG

Options

Select a spectra to compare to the spectra that is currently displayed. Options include:

- Display MRP - Displays the most-recent-prior sample.
- Blank - Displays a blank (unexposed filter) spectrum from the same station/detector combination as the currently displayed spectrum.
- Preliminary - Displays the PREL spectrum for the same sample as the currently displayed FULL spectrum.

- Closest - Allows an analyst to search for the closest match to the currently displayed spectrum. To query the database for the closest spectrum, click the Execute button. A search is made on the following:
  - Query - Search for Sample Time, Count Time, Decay Time, Flow Rate, or PB-212 Concentration.
  - Time - Select a time period.
- User Selected - Enter a sample number.
- Off.

Nuclide Review

The Nuclide Review window is made up of four graph windows and a nuclide selection list. When a nuclide is selected from the nuclide selection list or manually entered in the box provided, the spectral data points surrounding the four most abundant lines of the selected nuclide are displayed in the graph windows. The number of data points displayed for each line is enough to cover about 3.5 times the FWHM of the expected peak size (the expected peak size is computed from the resolution vs. energy regression [RER] equation). A 'pseudo-peak' is then overlaid on each graph to show approximately what the peak shape would be if the concentration of the selected nuclide was equal to the MDC (minimum detectable concentration). The analyst can then see the most abundant lines for the selected nuclide at one time

1. Choose Options> Nuclide Review.

   The Nuclide Review Window appears (Figure 15).

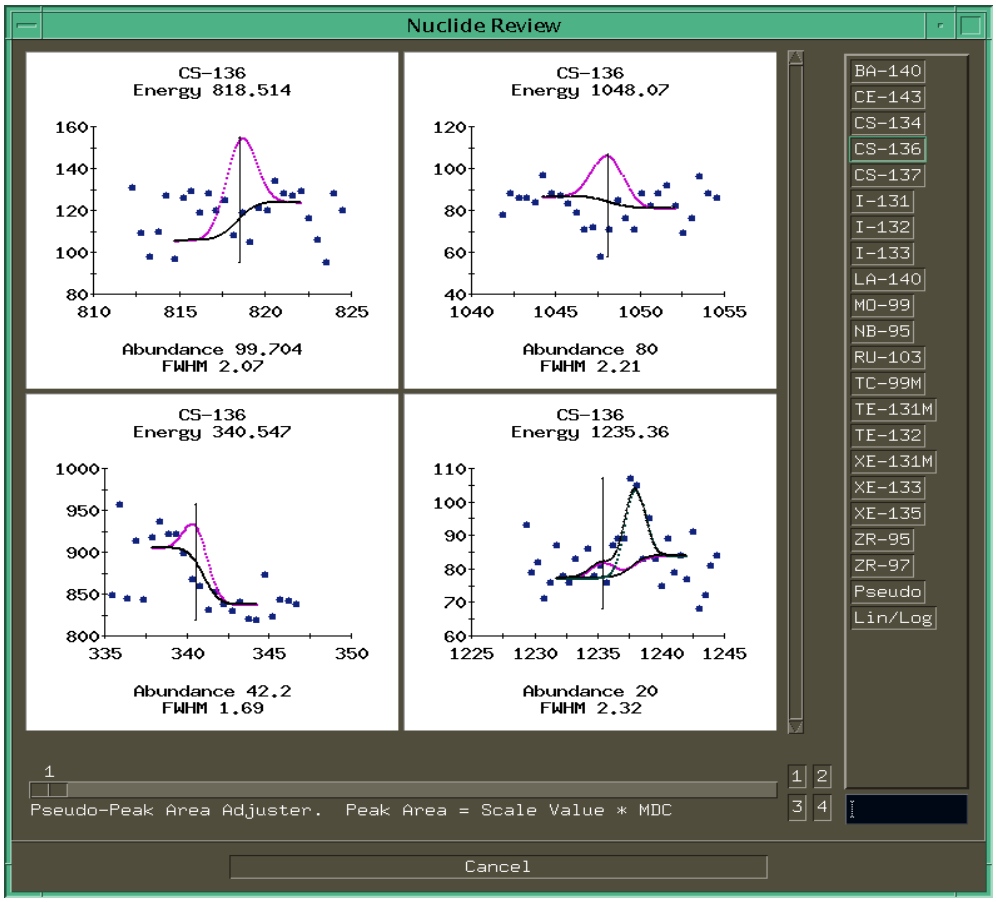


FIGURE 15. NUCLIDE REVIEW WINDOW

2. Click Cancel.

   You are returned to the Inspectra Tool window.

Residual Plot

The Residual Plot dialog provides a method for viewing the quality of a given peak fit. To use the residual plot tool, proceed as follows.

1. Choose Options>Residual Plot.

   The Residual Plot Window appears.

2. Click Cancel.

   You are returned to the Inspectra Tool window.

Peak Sig/PSS Plot

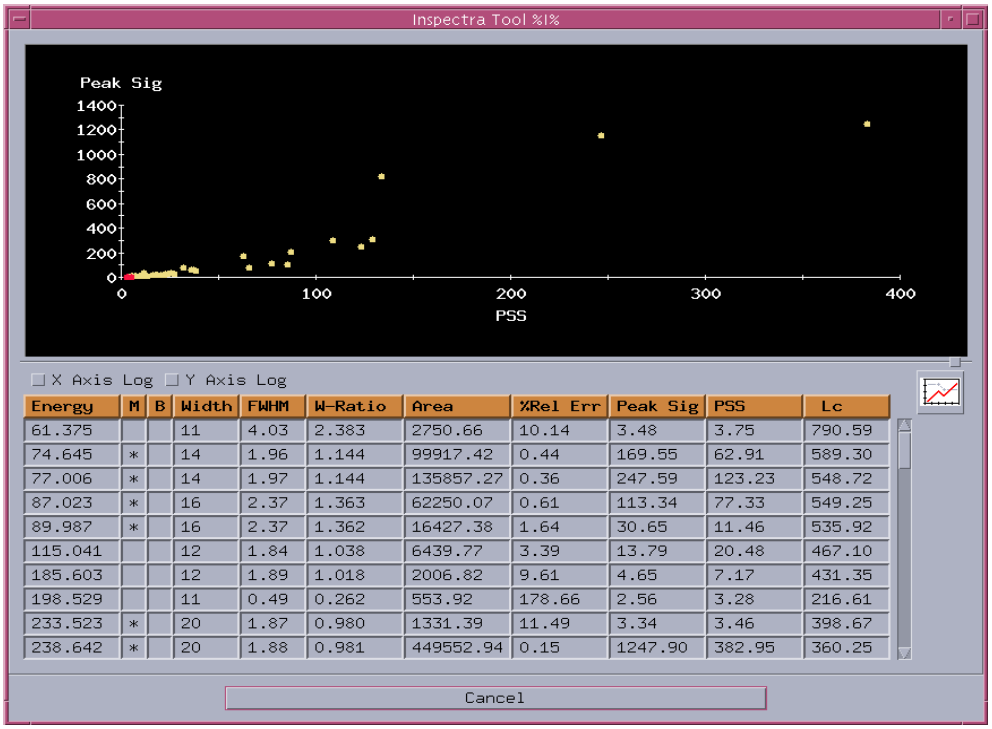
A scatter plot displaying the Canberra Peak Search Sensitivity (PSS) vs. the peak significance for each peak found during analysis is now available through Inspectra. This window also displays a table which contains the peak list and has the following columns: Energy, M (multiplet flag), B (background flag), Width (peak width in channels), FWHM (full width at half maximum), W-Ratio (FWHM ratio), Area, %Rel Err (percent relative uncertainty of peak area), Peak Significance, PSS, and Critical Level (Lc). The user can zoom into the plot by using SHIFT with the left mouse button. When a user selects a point on the scatter plot, the corresponding row in the table is highlighted. Like the Peak Search window, a toolbar button located next to the peak table allows the user to zoom into the graph area on the main Inspectra window.

1. Choose Options> Peak Sig/PSS.

   The Peak Search Sensitivity vs. Peak Significance Scatter Plot appears (Figure 16).

2. Click Cancel.

   You are returned to the Inspectra Tool window.



Energy	M	B	Width	FWHM	W-Ratio	Area	%Rel Err	Peak Sig	PSS	Lc
61.375			11	4.03	2.383	2750.66	10.14	3.48	3.75	790.59
74.645	*		14	1.96	1.144	99917.42	0.44	169.55	62.91	589.30
77.006	*		14	1.97	1.144	135857.27	0.36	247.59	123.23	548.72
87.023	*		16	2.37	1.363	62250.07	0.61	113.34	77.33	549.25
89.987	*		16	2.37	1.362	16427.38	1.64	30.65	11.46	535.92
115.041			12	1.84	1.038	6439.77	3.39	13.79	20.48	467.10
185.603			12	1.89	1.018	2006.82	9.61	4.65	7.17	431.35
198.529			11	0.49	0.262	553.92	178.66	2.56	3.28	216.61
233.523	*		20	1.87	0.980	1331.39	11.49	3.34	3.46	398.67
238.642	*		20	1.88	0.981	449552.94	0.15	1247.90	382.95	360.25

FIGURE 16. PEAK SEARCH SENSITIVITY VS. PEAK SEARCH SCATTER PLOT

Calibration Menu Selections

Table 5 provides an overview of the Calibration menu. Each selection is discussed in turn.

TABLE 5: CALIBRATION MENU SELECTIONS

Selection	Function
Equations	Displays calibration equations.
Pairs	Displays sample pulse height data pairs used in calibration equations.
Energy Function Plot	Graphically displays the deviation from perfect linearity in the energy versus channel regression (ECR) equation.
Resolution Function Plot	Graphically displays the resolution versus energy regression (RER) equation.
Efficiency Function Plot	Graphically displays the efficiency versus energy regression (EER) equation.

Equations

The Calibration Equation Dialog displays the ECR, RER, and EER equations.

Pairs

The Calibration Pair Dialog displays the data pairs used to compute the ECR, RER, and EER equations. This includes the energy-channel pairs, resolution-energy pairs, and efficiency-energy sent with the sample pulse height data (SPHD) file in the #g_Energy, #g_Resolution, and #g_Efficiency blocks.

Energy Function Plot

The Energy Function Plot Dialog, Figure 17, is a graphical display of the equation:

f(E) = ECR(E) - SLR_slope x E

where SLR_slope is the simple linear regression of the calculated ECR data points. The graph shows how the ECR deviates from a straight line. The error bars indicate the uncertainty in the energy location.

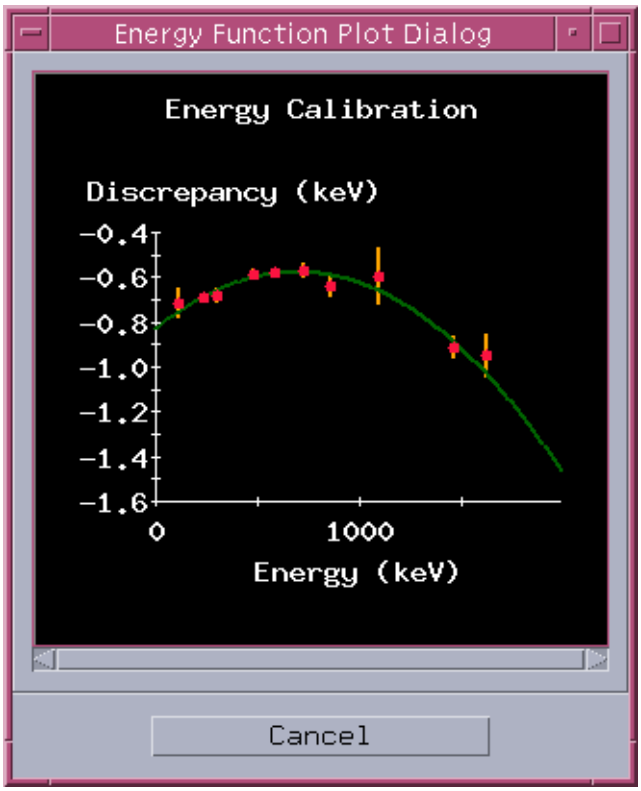


FIGURE 17. CALIBRATION ENERGY PLOT DIALOG

Resolution Function Plot

The Resolution Function Plot Dialog, Figure 18, is a graphical display of the RER equation. The error bars indicate the uncertainty in the FWHM. This display is helpful for viewing any irregularities in detector performance.

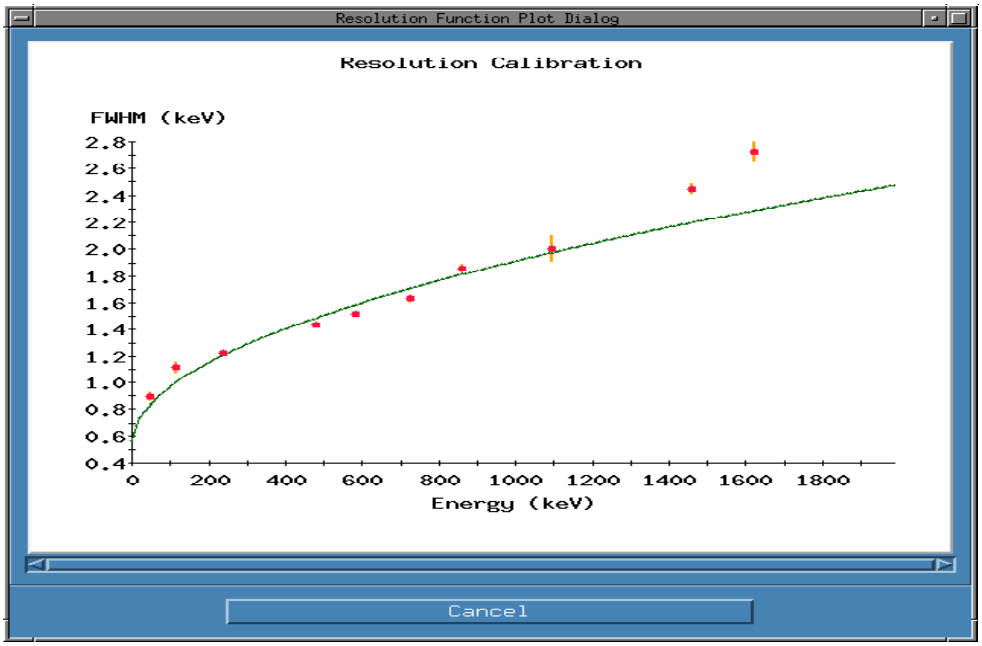


FIGURE 18. CALIBRATION RESOLUTION PLOT DIALOG

Efficiency Function Plot

The Efficiency Function Plot Dialog, Figure 19, graphically displays the EER equation The error bars indicate the uncertainty of the efficiency at a given energy. This window is helpful for viewing irregularities in detector performance.

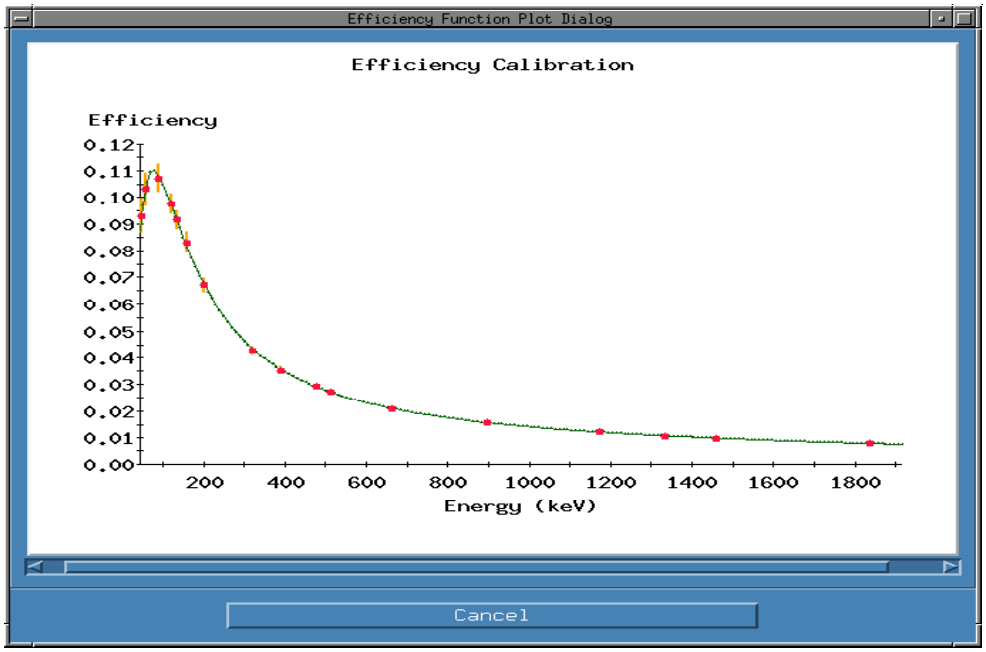


FIGURE 19. CALIBRATION EFFICIENCY PLOT DIALOG

Report Menu Selections

The Reports menu provides the selections discussed in Table 6.[2] Each report option is discussed in turn.

2. Although selections are active before a spectrum is selected, as in the Options and Calibrations menus, some options cannot provide information unless a spectrum is opened.

TABLE 6: REPORTS MENU SELECTIONS

Selections	Function
Peak Search	Displays all peak attributes and associated nuclides.
Peak Search Summary	Displays total number of lines found in the spectrum and total number of lines associated with nuclides.
Radionuclide Activity	Displays list of nuclides identified and/or quantified.
Categorization	Displays results from the prioritization or categorization process.
Minimum Detectable Concentration	Displays calculated MDC values for nuclides listed in the **gards_mdas2report** database table.
Sample Source	Displays station and detector details.
Sample Detail	Displays sample timing and other sample information.
Filename	Displays spectrum and sample pulse height data file names.
Nuclide Library	Displays the complete particulate or gas nuclide libraries, depending on the spectrum type.
ROI Comparison	Permits review of spectral ROI edits.
Data Quality Flags	Displays a list of data flag results (Pass/Fail).
Analysis Log	Displays the results from the automatic analysis process.
User Action Log	Displays the actions taken by the analyst during the spectrum review process.

Peak Search

The peak search window allows the user to see all peaks identified in the spectrum along with the nuclides associated with those peaks.[3] This window includes peak characteristics such as the centroid, area, area uncertainty, FWHM, and Critical Level (L_c) [Cur68].

To access this report, proceed as follows.

3. Through automated analysis, you can enter comments for each peak in the spectrum to identify Type I or Type II errors.

1. Choose Reports>Peak Search.

   The Peaks Search Dialog will appear.

2. Click Cancel.

   You are returned to the Inspectra Tool window

Peak Search Dialog Column Definitions

The following describes the columns in the Peak Search Dialog (Figure 20). Clicking on a column heading sorts records according to the data in that column .

- Energy: displays the actual energy location of a peak's midpoint.
- Centroid: displays the actual channel location of a peak's midpoint.
- M: An asterisk (*) in this column signifies multiple peaks in an ROI.
- B: displays whether blank subtraction effects the peak's net area.
- Width: displays the width of the ROI
- FWHM (Full Width Half Max): displays the resolution of a given peak.
- W-Rati. (W-Ratio): compares the width of a peak with that of the RER.
- Area: displays the net area of a peak.
- %RelErr: displays the percent relative error for each peak. This is approximately equivalent to the Poisson variability divided by the peak area and multiplied by 100. However, because the peaks are fitted, there are more components to this calculation. For details on the percent relative error calculation, see [Can95].
- Peak Sig: displays the ratio of peak area to $L_{C.}$ This allows comparison of the peak to the level and variability of the baseline.
- $L_{C:}$ displays the peak area above which a peak can be reliably recognized as detected at a given confidence level.
- #Cmnts: displays the number of comments an analyst made in that row. To show the entire column, click the column heading.

Selecting any row in this dialog activates the View Comments, Add Comment, Detector Contamination Comment, Modify Comment, View Lines, Remove Nuclide, Add Back Nuclide and Show Graph buttons located from top to bottom on the right side of the Peak Search Dialog window. (Figure 20). Each one of these buttons displays a “balloon help” feature were a text description of the button’s function pops up when the cursor is placed on top of the button. Below the action for each button is discussed.

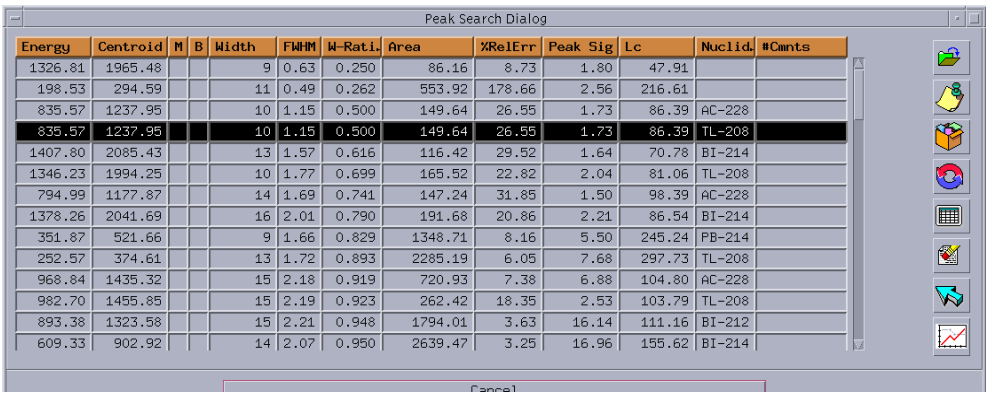


FIGURE 20. PEAK SEARCH DIALOG

View Comments

The View Comments button is the uppermost button, and when activated, displays comments that pertain to the highlighted row in the Peak Search Dialog.

1. Highlight a row that includes a number in the #Cmnts column.
2. Click the View Comments button to open the View Comments Dialog window.
3. Click Cancel to close the View Comments Dialog window.

Add Comment

To add a comment, proceed as follows.

1. Click the Add Comment button, located directly below the View Comments button.

   The Add Comments Dialog window appears, Figure 21. This window provides three comment binding options:

   – Click Energy to bind comments to every row in which that energy value appears in the Peak Search Dialog.
   – Click Nuclide to bind comments to every row in which the nuclide appears in the Peak Search Dialog.
   – Click Selected Row to bind comments to the row highlighted in the Peak Search Dialog.

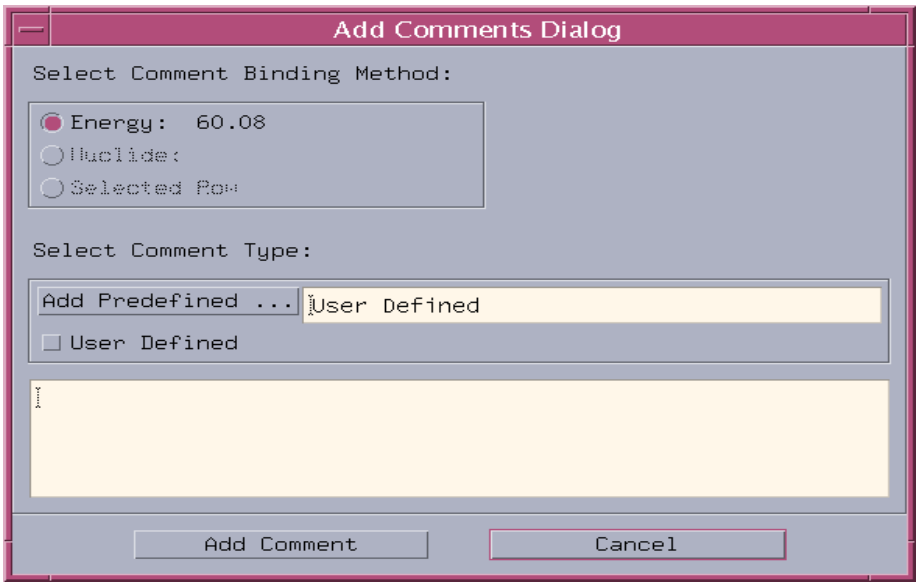


FIGURE 21. ADD COMMENT DIALOG

2. Select Comment Type

   There are two types of comments available: predefined or user-defined. Both types may be attached simultaneously.

To add a predefined comment, proceed as follows:

1. From the Add Comments Dialog window, click the Add Predefined button.

   A Predefined Comment Selection Dialog window appears.

2. Select one of the predefined comments from the list provided.
3. Click Add Comment.

   Your comment is added to the selected spectrum and you are returned to the Peak Search Dialog.

To add a User Defined comment, one of two methods can be used:

Method 1:

1. From the Add Comments Dialog window, click the Add Predefined button.
2. Click the User Defined button.
3. Select the empty text box and type comment(s).
4. Click Add Comment.

   Your comment is added to the selected spectrum and you are returned to the Peak Search Dialog.

Method 2:

1. In the Add Comments Dialog, click the User Defined button.
2. Select the empty text box and type comments.
3. Click Add Comment.

   Your comment is added to the selected spectrum and you are returned to the Peak Search Dialog.

Detector Contamination Comment

This interface allows the analyst to simultaneously remove a nuclide from the Activity Summary section of the RRR and attach a predefined detector contamination comment to all lines in the peak search results associated with that nuclide.

To attach a detector contamination comment, proceed as follows:

1. Click the Detector Contamination Comment button (third button from the top).

   A Detector Contamination Comment window appears and displays a prompt, "Add a detector contamination comment and remove nuclide?"

2. Click Yes.

The nuclide is removed from the Activity Summary section of the RRR; however, it is still included in the Peak Search section of the RRR, and the following comment is attached to the #Cmnts column for all lines associated with that nuclide:

```
This radionuclide is present in the spectrum but it
results from detector contamination.  Therefore, it has
been removed from the atmospheric radionuclide activity
summary.
```

Modify Comment

This interface allows an analyst to modify or delete their peak comments. The new window only allows an analyst to modify comments during the review process. Once a sample is released, the comment may no longer be changed using this window. The window also prohibits an analyst from modifying another analyst's comments or one of the predefined comments.

To modify a comment, proceed as follows:

1. Click the Modify Comment button (the fourth button from the top).

   The Modify Comments Dialog appears (Figure 22). This dialog provides three comment options:

   – Delete. The comment is deleted.
   – Same. The comment remains the same.
   – Modify. The comment can be modified.

2. Commit or cancel the modifications by clicking the Save or Cancel button, respectively.

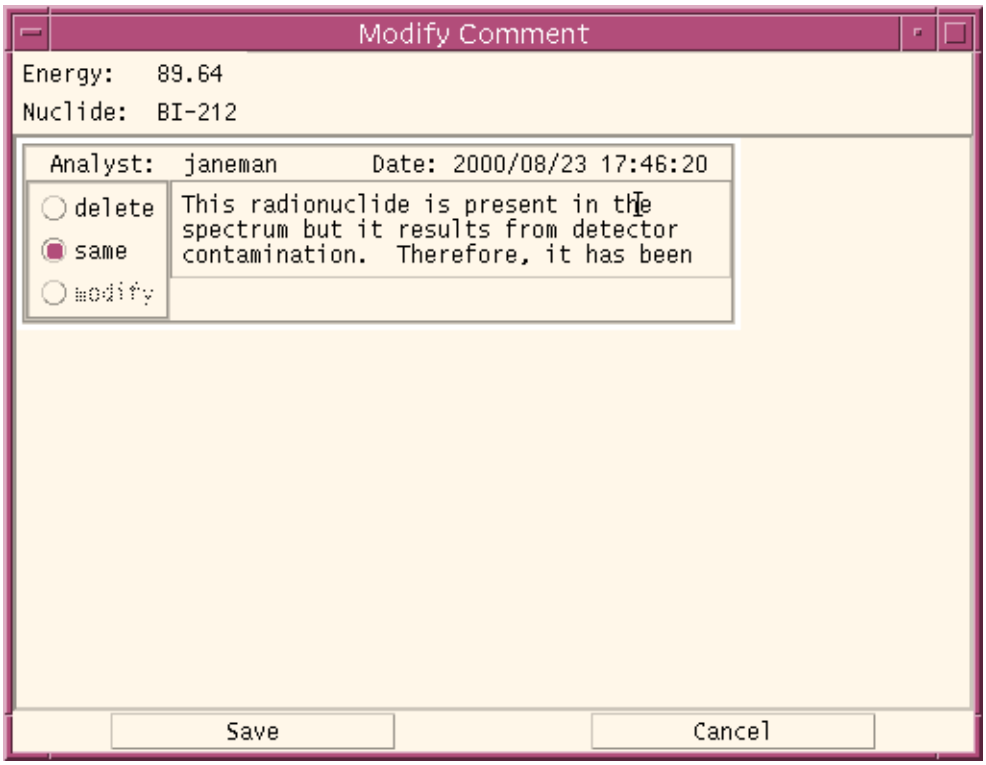


FIGURE 22. MODIFY COMMENT DIALOG

View Line Activity

In the Reports Peak Search Dialog, highlight a row with an entry in the Nuclide column. Click the View Line Activity button (fifth button from the top) and the Nuclide Lines Activity Dialog will appear (Figure 23).

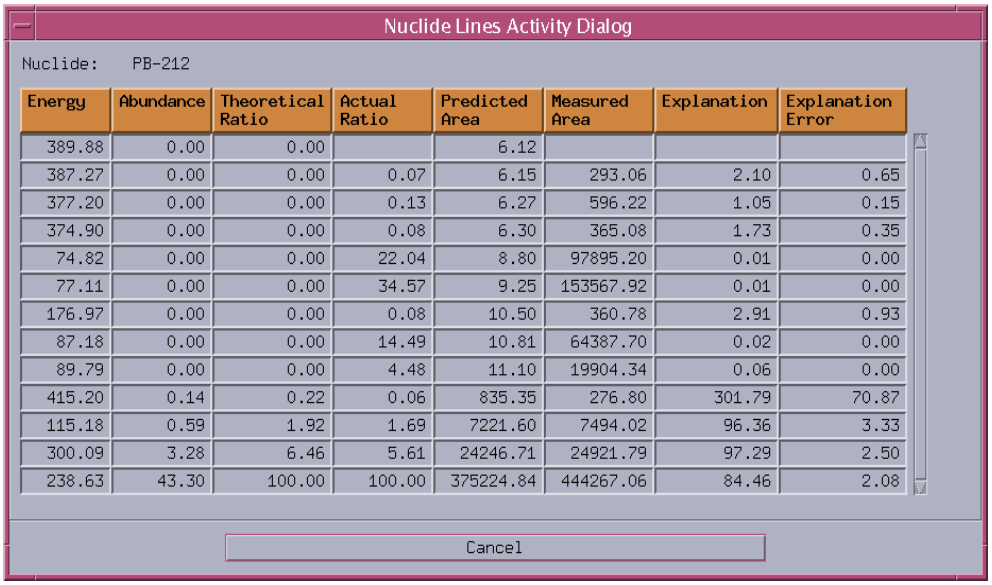


FIGURE 23. NUCLIDE LINES ACTIVITY DIALOG

Nuclide Lines Activity Dialog Features

The Nuclide Lines Activity Dialog displays additional automatic processing information used for nuclide identification. The following parameters are included in the window: Energy, Abundance, Theoretical Ratio, Actual Ratio, Predicted Area, Measured Area, Explanation, and Explanation Error.

The following features are available in the Nuclide Line Activity Dialog:

- Clicking the column heading sorts according to the data in that column.
- The Nuclide Lines Activity Dialog displays data for selected nuclides without being closed and reopened. This enables you to return to the Peak Search Dialog and highlight other rows having entries in the Nuclide column.

The Energy and Abundance columns provide the energy and abundance of the specified nuclide. The Theoretical Ratio column displays the product of each photon's efficiency and abundance normalized to the results for the photon line with the largest product of these two numbers. The Actual Ratio column is the peak area for each photon divided by

the peak area of the photon with the largest value for the theoretical ratio (expressed as a percent). The peak with the largest theoretical ratio will always have an actual ratio of 100 percent.

The Predicted Area is calculated using the nuclide average activity, the abundance, and efficiency corrected for collection, decay and acquisition time. The Measured Area displays the peak area if the peak is present in the spectrum. The average activity is used since this value includes corrections for interferences when it is calculated.

The Explanation column shows the ratio of the predicted area to the actual area in percent; the Explanation Error includes the uncertainty of this ratio.

Note that changes made to the abundance levels in the nuclide library will affect these calculations.

Remove Nuclide

To remove a nuclide, proceed as follows.

1. Click the Remove Nuclide button (the sixth button from the top).

   The Remove Nuclide Confirmation Dialog appears and displays a prompt, `“Unflag Nuclide from Activity Summary?”`

2. Click Yes.

   The nuclide is removed from the Activity Summary section of the RRR. It is, however, included in the Peak Search section of the RRR, and the following comment is automatically attached to the #Cmnts column:

   ```
   This nuclide was removed from the Activity Summary section because, in the analyst’s judgment, the nuclide was not present; some nuclides can be removed because their activity calculations are not meaningful (they are not identified, not quantified.)
   ```

Add Back Nulcide

This button allows the operator to add back a nuclide that was erroneously deleted or removed. When the button is clicked and the corresponding nuclide row is highlighted, a dialog box appears requesting confirmation of this action. Once the action is confirmed, a comment is generated stating the nuclide was erroneously removed and this comment is stored in the database. In addition, the Nuclide Id flag in the **gards_nucl_ided** table is updated and reset to show the nuclide has been identified.

Show Graph

Press this button to reveal a graph of the selected peak in the main Inspectra display window. The button is located at the lower right corner of the Peak Search Dialog window.

Peak Search Summary

The Peak Search Summary provides a summary of the spectrum analysis results. This summary includes the number of lines found, the number of lines associated with nuclides, the number of lines not associated with nuclides, and the percent of associated lines.

To select the Peak Search Summary, proceed as follows:

1. Choose Reports>Peak Summary.

   The Peak Search Summary Dialog appears.

2. Click Cancel.

   You are returned to the Inspectra Tool window.

Radionuclide Activity

This report provides radionuclide activity data. Its features are discussed in "Radionuclide Activity Dialog Features" on page 74. To access this report, proceed as follows.

1. Choose Reports>Radionuclide Activity.

   The Radionuclide Activity Dialog appears (Figure 24).

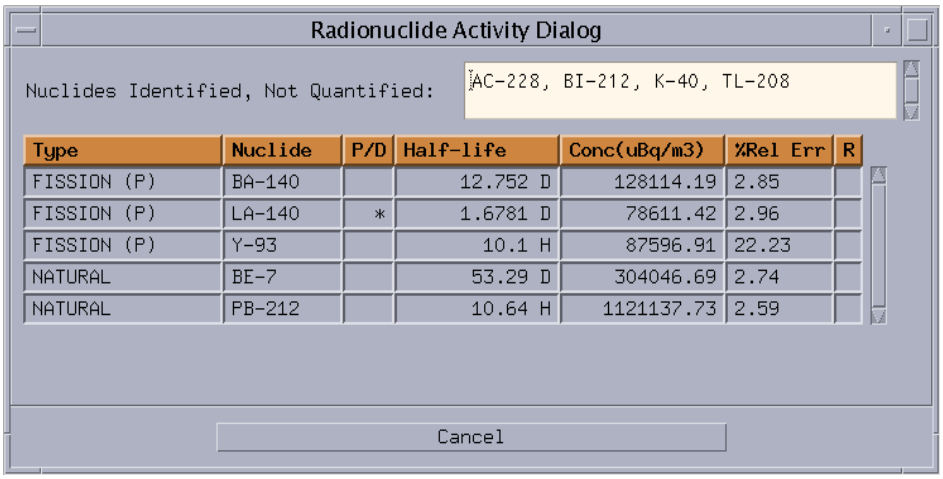


FIGURE 24. RADIONUCLIDE ACTIVITY DIALOG

2. Click Cancel.

   You are returned to the Inspectra Tool window.

Radionuclide Activity Dialog Features

The Radionuclide Activity selection provides the following features:

- Clicking a column heading sorts rows according to the data in that column.
- The Type column lists radionuclides according to the five types in the nuclide library: ACTIVATION, FISSION (P), FISSION (G), COSMIC, and NATURAL. Each of these radionuclide types are described in "Library Data Characteristics" on page 83.
- An asterisk in the P/D (parent/daughter) columns means that the keyline concentration for the nuclide was modified during the parent/daughter calculations.
- Half-lives are shown in the units Y (year), D (day), and H (hour).
- Concentration (Conc) is in micro Bequerels per cubic meter ($\mu Bq/m^3$).

- The percent relative error (%Rel Err) column contains the concentration uncertainty in percent. It includes contributions from all of the components of the activity concentration that are subject to measurement error. The activity error is dominated by the net peak area uncertainty. See [Can95] for details on percent relative error calculations.
- An asterisk in the R (Removed) column means the nuclide has been removed and it will not appear in the Activity Summary section of the RRR. After clicking Remove Nuclide in the Peak Search Dialog, and selecting Yes in the Remove Nuclide Confirmation Dialog, an asterisk (*) appears in that nuclide's column of the Radionuclide Summary.

Categorization

The Categorization Dialog, Figure 25, displays the results from the automatic prioritization process. The sample prioritization levels are as follows:

- Level 1. Spectrum contains natural and/or anthropogenic radionuclides not on the categorization list for particulate samples (CLPS) that are within the normally observed range for the station. A natural radionuclide with no pre-established filter would also generate a Level 1 categorization. (If no radionuclides are identified in a spectrum, it is categorized as Level 1.)
- Level 2. Spectrum contains natural and/or anthropogenic radionuclides not on the CLPS that are either not normally observed at the station, or are outside of the normally observed range. Xenon samples may not be categorized as Level 2, since the only radionuclides quantified are on the categorization list.
- Level 3. Spectrum contains anthropogenic radionuclides on the CLPS (relevant fission or activation products) that are within the normally observed range for the station.
- Level 4. Spectrum contains anthropogenic radionuclides on the CLPS that are not normally observed at the station or are outside of the normally observed range.

- Level 5. Spectrum contains multiple anthropogenic radionuclides on the CLPS that are outside normal observations, or does not have a pre-established filter, and at least one of the anthropogenic nuclides is a fission product.

To access the Categorization report, proceed as follows:

1. Choose Report>Categorization.

   The Categorization Dialog appears.

2. Click Cancel.

   You are returned to the Inspectra Tool window.

Categorization Dialog Features

The Categorization Dialog, Figure 25, permits review of the interactive categorization results. Clicking the heading of a specific column sorts the rows in the table according to the data in that column in ascending order.

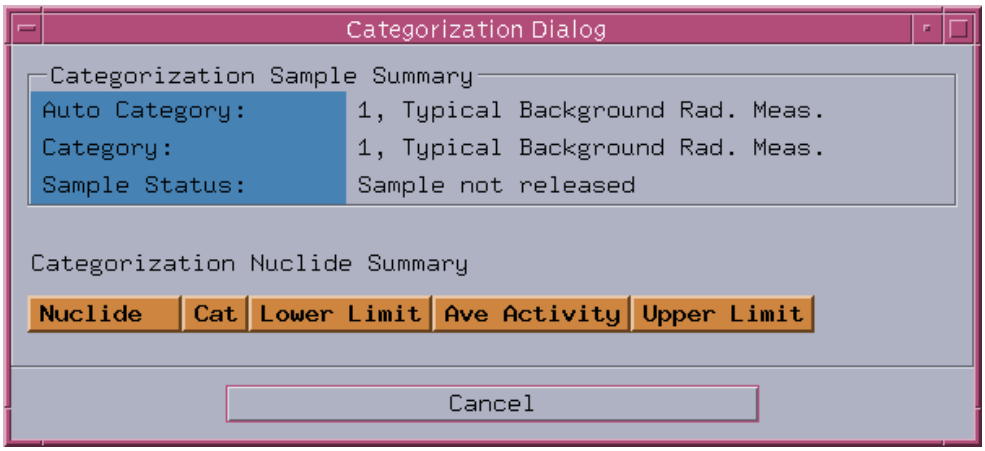


FIGURE 25. CATEGORIZATION DIALOG

Prioritization Requirements

There are several requirements associated with the automatic prioritization processing. These are listed below.

- Statistical filters need to be established for each new station.
- When station characteristics change, statistical filters need to be reinitialized.
- Samples must be released in chronological order for the EWMA categorization filter to work properly. If station operating procedures make this impossible to achieve, then the statistical filters may need to be reinitialized.

Minimum Detectable Concentration (MDC)

The Minimum Detectable Concentration (MDC) dialog, Figure 26, displays the fission and activation products listed in the **gards_mdas2report** database table. The MDC values are unique to each spectrum and are calculated during the automatic analysis process for all nuclides in the nuclide library. The Min MDC and Max MDC values are static for all spectra. Clicking the heading of a specific column sorts the rows in the table according to the data in the column. Numerical data is sorted in ascending order.

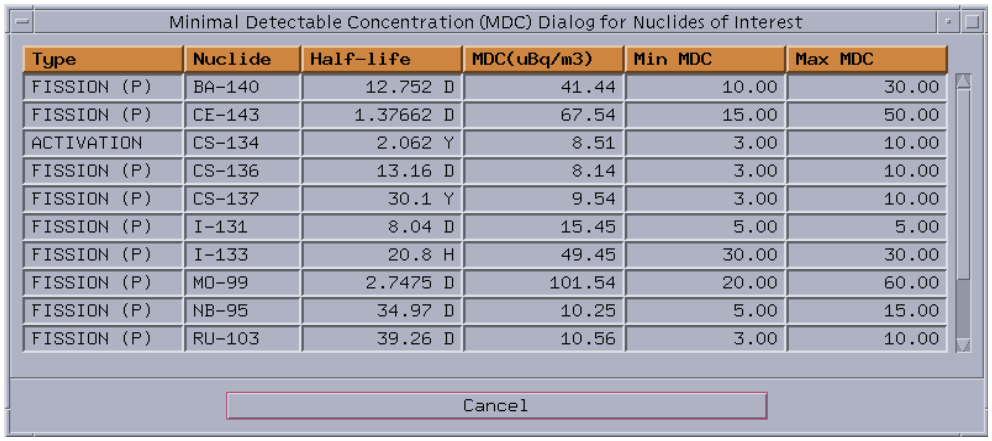
To access the MDC dialog, proceed as follows.

1. Choose Reports>Minimum Detectable Concentration.

   The Minimum Detectable Concentration (MDC) Dialog window appears.

2. Click Cancel.

   You are returned to the Inspectra Tool window.



Type	Nuclide	Half-life	MDC(uBq/m3)	Min MDC	Max MDC
FISSION (P)	BA-140	12.752 D	41.44	10.00	30.00
FISSION (P)	CE-143	1.37662 D	67.54	15.00	50.00
ACTIVATION	CS-134	2.062 Y	8.51	3.00	10.00
FISSION (P)	CS-136	13.16 D	8.14	3.00	10.00
FISSION (P)	CS-137	30.1 Y	9.54	3.00	10.00
FISSION (P)	I-131	8.04 D	15.45	5.00	5.00
FISSION (P)	I-133	20.8 H	49.45	30.00	30.00
FISSION (P)	MO-99	2.7475 D	101.54	20.00	60.00
FISSION (P)	NB-95	34.97 D	10.25	5.00	15.00
FISSION (P)	RU-103	39.26 D	10.56	3.00	10.00

FIGURE 26. MINIMUM DETECTABLE CONCENTRATION DIALOG.

Minimum Detectable Concentration Dialog Features

The following describes features of this dialog:

- Data are easily sorted by clicking the heading of a given column.
- To change the list of fission or activation products displayed in this window, refer to “Data Workbench Procedures” on page 173.

Sample Source

The Sample Source Dialog, Figure 27, displays station and detector details. These data originate from the **gards_stations** and **gards_detectors** database tables.

To access this report, proceed as follows.

1. Choose Report>Sample Source.

   The Sample Source Dialog appears.

2. Click Cancel.

   You are returned to the Inspectra Tool window.

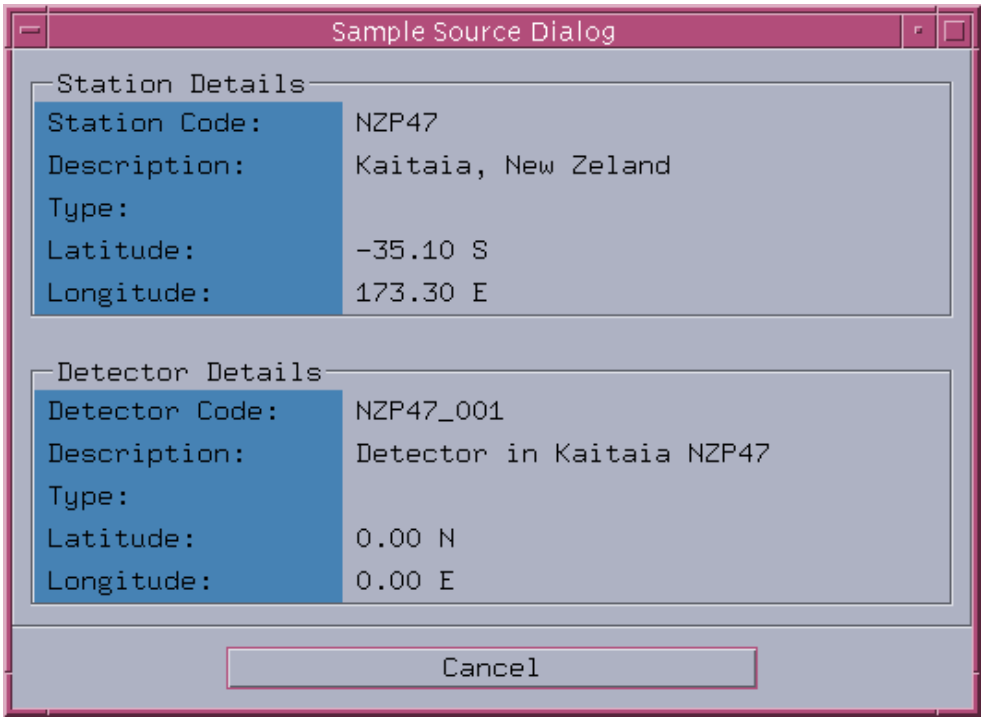


FIGURE 27. SAMPLE SOURCE DIALOG

Sample Detail

The Sample Detail Dialog (Figure 28) provides sample overview and sample timing information. The average values indicated in the Quantity, Sampling Time, Decay Time, and Acquisition Time fields are derived from that station's historical data.

To access this report, proceed as follows:

1. Choose Reports>Sample Detail.

   The Sample Detail Dialog appears.

2. Click Cancel.

   You are returned to the Inspectra Tool window.

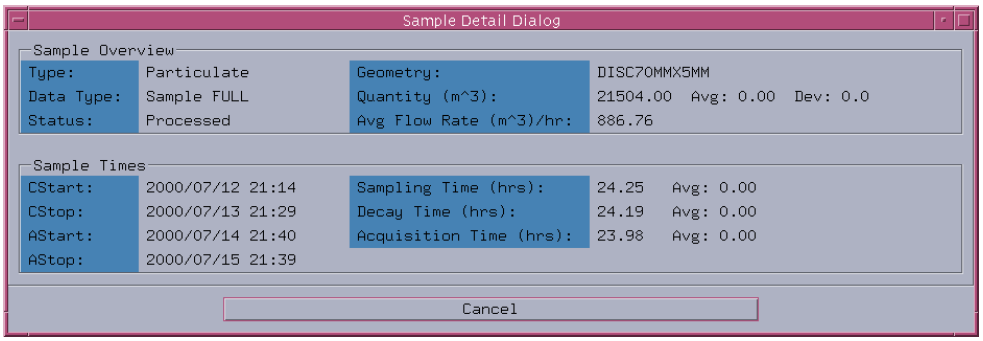


FIGURE 28. SAMPLE DETAIL DIALOG

Filename

The Filename Dialog, Figure 29, displays the disk locations for the SPHD and Spectrum flat files. SPHD files contain the raw data sent from the collection sites. Spectrum files contain the data in the #Spectrum block.

To access this report, proceed as follows:

1. Choose Reports>Filename.

   The Sample Filename Dialog appears.

FIGURE 29. SAMPLE FILENAME DIALOG

2. To display the entire filename, resize the window by selecting the lower left or right corner of the table (an arrow and a square edge appear). Drag the corner until the dialog is an appropriate size.
3. Click Cancel.

   You are returned to the Inspectra Tool window.

Nuclide Library

The Nuclide Library Dialog (Figure 30) provides access to the information used for nuclide identification, and is a primary aid to the analyst in researching unidentified lines in a spectrum. The Nuclide Library Dialog will automatically display either the particulate or xenon library, depending on the sample type of the spectrum selected.

To access the Nuclide Library report, proceed as follows.

1. Choose Reports>Nuclide Library.

   The Nuclide Library Dialog appears. For a discussion of Library Features see page 82; for Library Data Characteristics see page 83; and for Library Sorting Features see page 84.

   The Nuclide Library consists of three tables. The first table (shown in the upper portion of the Nuclide Library Dialog) and the combined two tables in the lower portion of the window have the following columns: Energy, Nuclide, Abundance, Type, Half-life, and True Half-life. The first table lists all the photon lines found in the nuclide library, in ascending order. The lower left table lists all the radionuclides in the library, in alphabetical order. The lower right table lists all the energy lines and corresponding abundances, in descending order of abundance, associated with a nuclide selected from the lower left table.

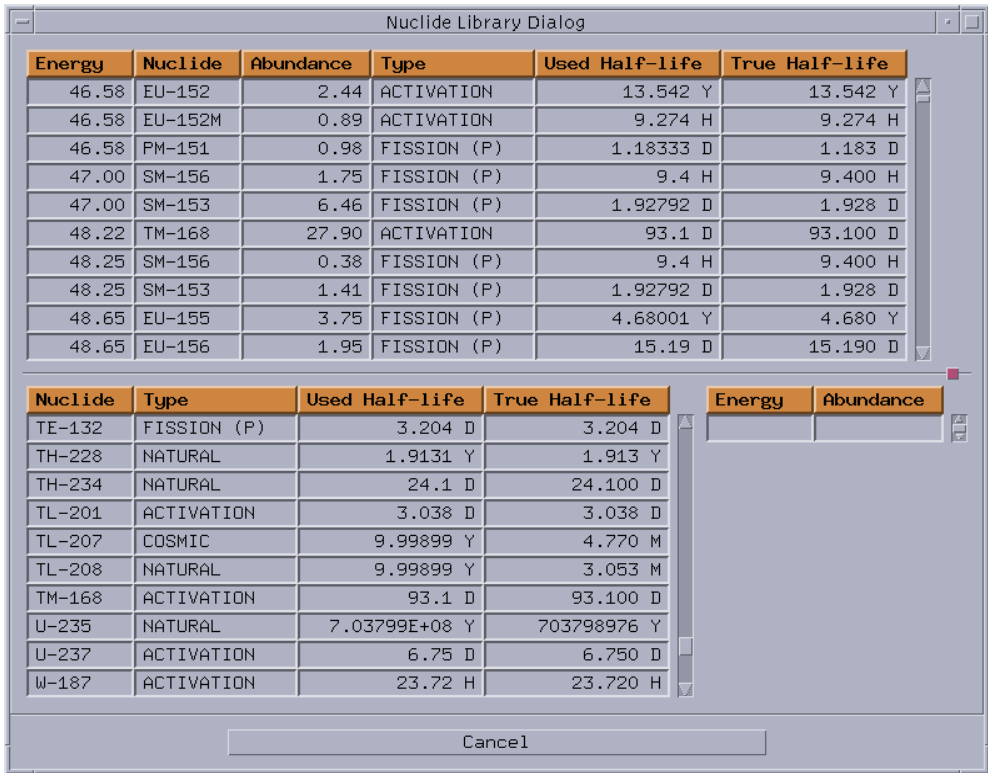


FIGURE 30. NUCLIDE LIBRARY DIALOG

2. Select a row in the lower left table.

   This activates the lower right table, but no further commands or events follow.

3. Click Cancel.

   You are returned to the Inspectra Tool window.

Library Features

The features of the Nuclide Library are described below.

- The size of the upper and two lower tables in the Nuclide Library Dialog can be changed. To adjust these tables, proceed as follows.

- Place the pointer on the small square button beneath the uppermost table's right scroll bar so that the pointer changes to a crosshair.
- Click the square button, dragging upward or downward.

- Keyboard commands do not apply to the Nuclide Library.

Library Data Characteristics

Characteristics of the nuclide library data are described below.

- Energy - This is the photon energy given in keV.
- Nuclide - The first table (shown in the upper portion of the window) displays a nuclide by each of its associated photon energies. The lower left table lists a nuclide once, while the table to the right displays the energies and abundances associated with the photons of that nuclide.
- Abundance - The abundance is the fraction of decays that result in the emission of the photon line of interest. Its units are photons/disintegration, but are often quoted as a fraction or percent.
- Type - This column displays five possible labels for a given nuclide.
  - Activation - These are nuclides that result from neutron activation reactions.
  - Fission (P) - These are particulate fission products.
  - Fission (G) - These are gaseous fission products.
  - Cosmic - These are nuclides produced by the interaction of cosmic-rays with matter.
  - Natural - Nuclides that are found naturally in the environment, not man-made.
- Used Half-life. This is the time used in the calculations for the radionuclide to decay to half its initial activity. Some of the natural nuclides are assigned an artificial half-life of 9.999 Y, which is simply a flag value. Nuclides with this artificial half-life are identified, but not quantified by the automated processing. The following suffix labels are used in this column:
  - M for minutes.

  - H for hours.
  - D for days.
  - Y for years.
- True Half-life. This is the actual half-life for that particular nuclide as derived from the **gards_aux_lib** table

Library Sorting Features

The sorting features of the Nuclide Library are described below.

- Click the heading of any column to sort data in ascending order.
- When sorting a column, the vertical scroll bars for that table do not return you to the data at the top of the table; therefore, manual scrolling might be necessary to get to the location of interest after each sort

Analysis Log

The Analysis Log window, Figure 31, provides the step-by-step results from the automatic analysis process from the start of the analysis to its completion. The analyst must become familiar with the steps involved in the automatic analysis process to thoroughly understand the records of the analysis log output.

To access the Analysis Log report, proceed as follows.

1. Choose Report>Analysis Log.

   The Analysis Log window appears.
2. Click Cancel.

   You are returned to the Inspectra Tool window.

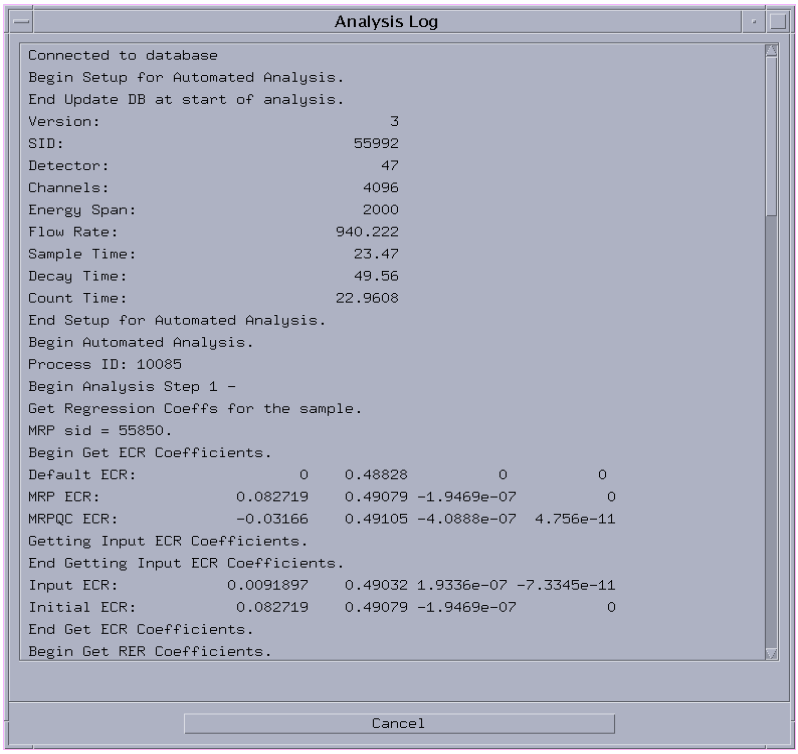


FIGURE 31. ANALYSIS LOG

User Action Log

The User Action Log, Figure 32, window provides the step-by-step actions taken by the analyst during the review process. The records are ordered from the start of the review process to its completion. All actions taken by the analyst are recorded.

To access the User Action Log report, proceed as follows.

1. Choose Report>User Action Log.

   The User Action Log window appears. Use the Reload button to update the display.

2. Click Cancel.

   You are returned to the Inspectra Tool window.

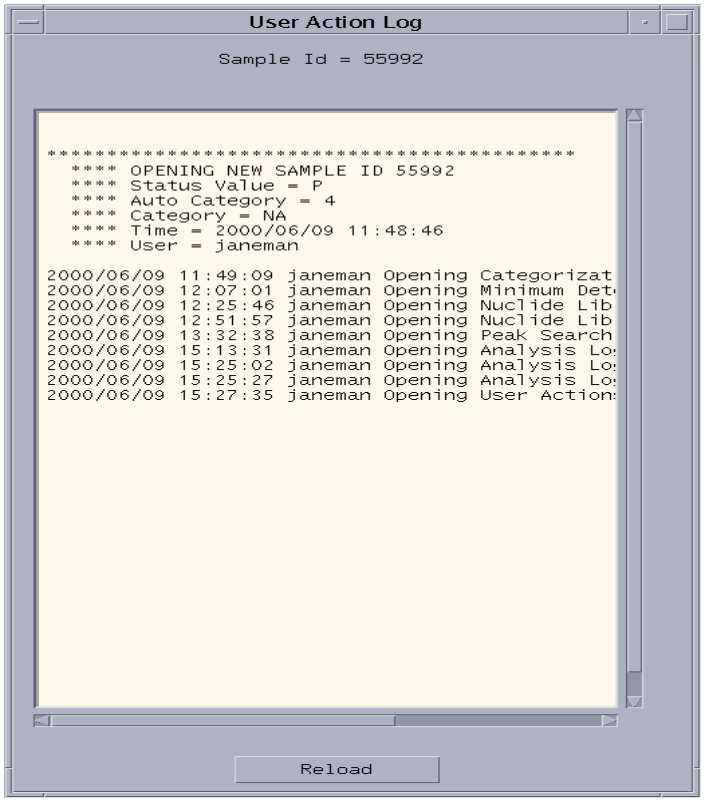


FIGURE 32. USER ACTION LOG

Region of Interest Comparison

The Region of Interest Comparison Dialog, Figure 33, allows you to review edits made to a spectral region of interest (SROI). Results are shown for Peaks Added, Peaks Deleted, SROIs Modified, and Nuclide-ID Changes. These data provide specific information about the type of edits made to peaks in an SROI. The Nuclide-ID Changes provides additional spectral data, such as the following.

- Average Concentration Differences. This list contains the nuclides whose concentrations changed as a result of the interactive review process.

- Nuclides entering. This list describes nuclides inserted during the interactive review process.
- Nuclides leaving. This list describes nuclides deleted during the interactive review process.

To access this window, proceed as follows.

1. Choose Reports>Region of Interest Comparison.

   The ROI Comparison Dialog appears.

2. This window may not be edited. If additional changes are required, choose Options>ROI and proceed with edits.

3. Click Cancel.

   You are returned to the Inspectra Tool window.

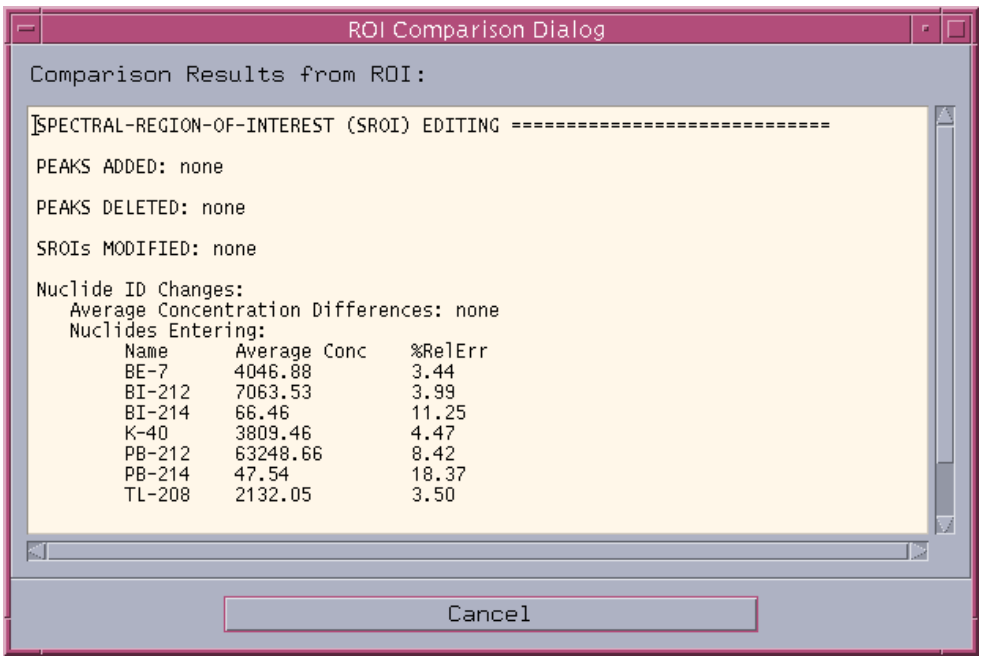


FIGURE 33. ROI COMPARISON DIALOG

Data Quality Flags

The Data Quality Flags window, Figure 34, summarizes the results from the data flags process. The data quality tests compare the sample specific flow rate, ^{140}Ba_MDC, ^{7}Be_FWHM, ^{40}K_location difference, and the Normalized Gain Difference values to specific threshold values. Details of these tests are described in [IDC5.2.2Rev2].

Note that new timeliness flags have been added to the Inspectra Data Quality Flags window as shown in Figure 35 below.

To access this window, proceed as follows.

1. Choose Reports>Data Quality Flags.

   The Data Quality Flags window appears.

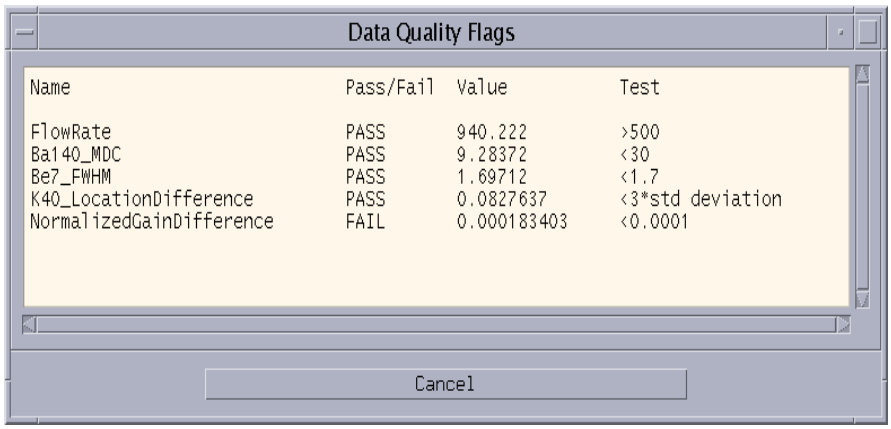


FIGURE 34. DATA QUALITY FLAGS

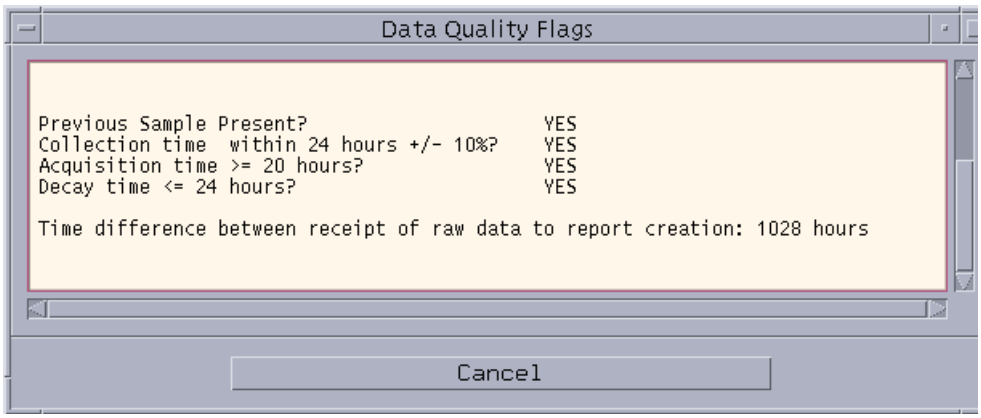


FIGURE 35. DATA QUALITY FLAGS - TIMELINESS FLAGS

2. Click Reload to update the display.
3. Click Cancel.

   You are returned to the Inspectra Tool window.

Processing Menu Selections

Processing menu selections are shown in Table 7. Each process is discussed in turn.

TABLE 7: PROCESSING MENU SELECTIONS

Selections	Function
Processing Parameters	Displays the processing parameters used for spectral analysis.
Update Processing Parameters	Displays the update processing parameters used for spectral analysis.

TABLE 7: PROCESSING MENU SELECTIONS (CONTINUED)

Selections	Function
Analyze Sample	Analyzes sample that has not been processed through the pipeline.
Mark Released	Marks a sample to be released to post-analysis processing and initiates the calculation for review time.
Add General Comment	Provides additional explanation for actions taken during the interactive analysis of a sample.

Processing Parameters

The Processing Parameters Dialog, Figure 36, displays the processing parameters that were used for spectral analysis. See [IDC5.2.2Rev2] for more information.

To access the Processing Parameters dialog, proceed as follows.

1. Choose Processing>Processing Parameters.

   The Processing Parameters Dialog appears.

2. Click Cancel.

   You are returned to the Inspectra Tool window.

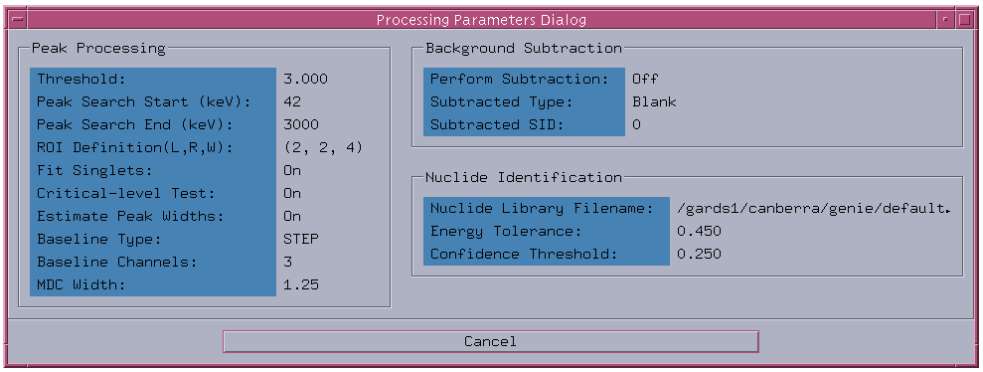


FIGURE 36. PROCESSING PARAMETERS DIALOG

Update Processing Parameters

The Update Processing Parameters Dialog, Figure 37, displays the update processing parameters that were used during spectral analysis. See [IDC5.2.2Rev2] for more information.

To access the Processing Parameters dialog, proceed as follows.

1. Choose Processing>Update Processing Parameters.

   The Processing Parameters Dialog appears.

2. Click Cancel.

   You are returned to the Inspectra Tool window.

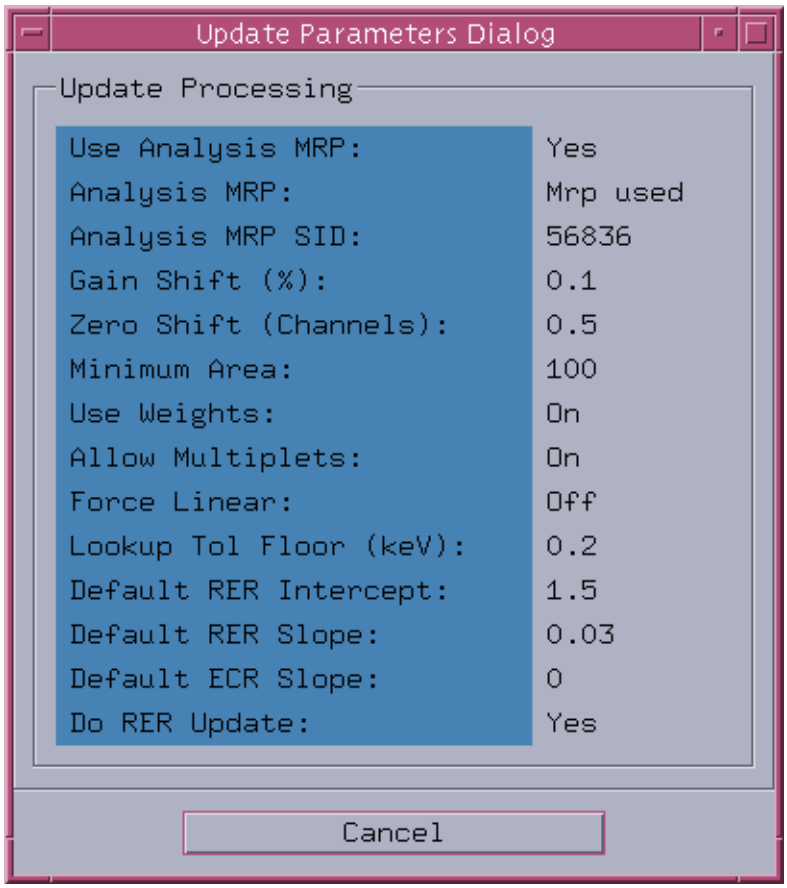


FIGURE 37. UPDATE PROCESSING PARAMETERS DIALOG

Parameter Override Window [(Re) Process Sample]

The Parameter Override Window (POW), Figure 38. is an interactive GUI that permits the user to change processing parameters and re-analyze samples with new parameter values. The values presented in the POW are described in Table 8. See [Bro94a], [IDC5.1.1Rev3], and [IDC5.2.2Rev2]for more information.

TABLE 8: PARAMETER OVERRIDE WINDOW VALUES

Parameter	Description
Update Parameters	*Parameters used to update the ECR and RER calibrations during analysis.*
Gain Shift	Gain change for matching energy calibration.
Zero Shift	Zero change for matching energy calibration.
Area Lim	Minimum peak area for inclusion in matching.
Min_lookup	Minimum lookup tolerance (keV).
Use Weight	Flag for use of weights in ECR updating.
Use Mult	Flag for use of multiplets in ECR updating.
Do_RERU	Flag to perform RER update after ECR update.
F Linear	Forces linear fit of ECR calibration.
Bootstrap	Flag to ignore prior ECR and RER calibrations
Processing Parameters	*Parameters used in automatic analysis for peak search and nuclide identification.*
FWHM_Mult_Width	FWHM to use in determining multiplets.
Left_FWHM_Lim	Left ROI FWHM limit.
Right_FWHM_Lim	Right ROI FWHM limit.
Peak_Start	Energy at which peak search starts (keV).
Peak_End	Energy at which peak search ends (keV).
NID_Confid	Nuclide identification confidence factor.
Peak_Sense	Peak search sensitivity.
Back_Chan	Number of continuous channels to the right and left of an ROI used to determine the background counts.
Nuclide_Lib	Nuclide library used for analysis.
MDA_Level	MDA confidence factor.
MDC_Width	Baseline width used for MDC calculation.
Energy_Tol	Energy tolerance.

TABLE 8: PARAMETER OVERRIDE WINDOW VALUES (CONTINUED)

Parameter	Description
lc_abscissa	Abscissa of the normal distribution corresponding to a confidence level. (A value of 1.645 corresponds to a 95% confidence.)
Back_Type	Background type: STEP or LINEAR.
Back_Data_Type	PHD type used for background subtraction (B for BLANKPHD and D for DETBKPHD).
Do_Back	Flag to perform background subtraction.
Fit_Singlets	Flag to fit singlets.
Fix_FWHM	Flag to fix the width of the fitted peaks to those defined in the RER.
Crit_level	Flag to perform critical level test.
Area_reject	Flag to reject zero area peaks.
Pd_Calc	Flag to perform parent-daughter calculations.
ECR	*Energy vs. channel regression parameters.*
b1	First order calibration coefficient (y intercept).
b2	Second order calibration coefficient (slope).
b3	Third order calibration coefficient.
b4	Fourth order calibration coefficient.
RER	*Resolution vs. energy regression parameters.*
b1	First calibration coefficient.
b2	Second calibration coefficient.
b3	Third calibration coefficient (not currently used).

To access the Parameter Override Window, proceed as follows.

1. Choose Processing>(Re)Process Sample.

   The POW appears. The POW enables the user to alter update parameters, processing parameters, ECR coefficients, and RER coefficients through the use of text fields and toggle buttons and reanalyze the sample by clicking the Analyze button.

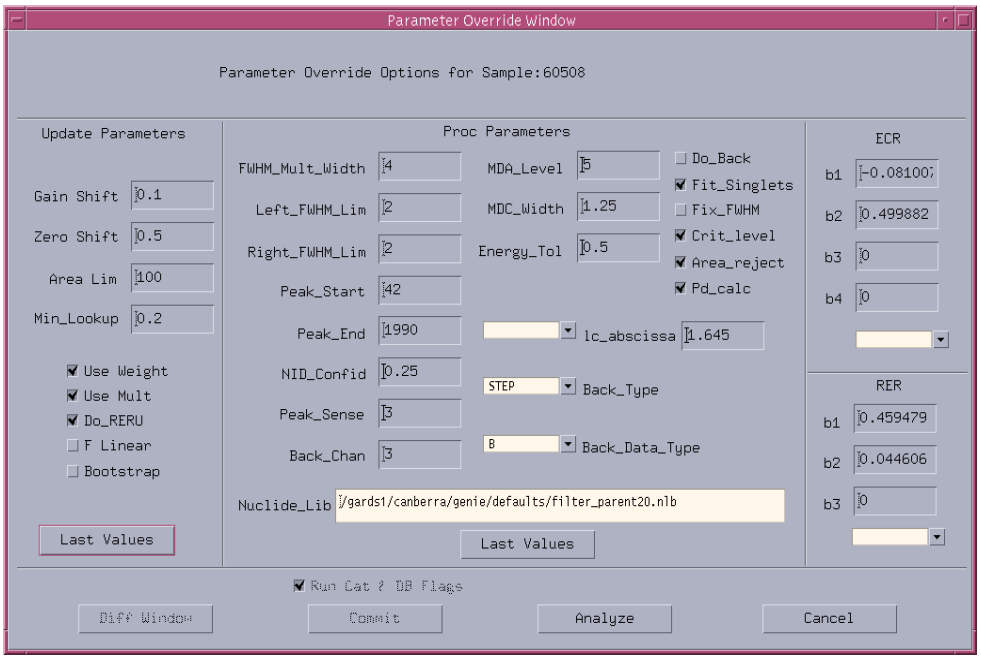


FIGURE 38. PARAMETER OVERRIDE WINDOW

2. Click Commit to update the database after reanalysis.

   This action will run the categorization and database flags routines by default, but these options may be turned off by manipulating the toggle button located above the Commit button. Updates to the database do not include modification to any of the **gards_orig** tables.

3. Click Cancel.

   You are returned to the Inspectra Tool window.

Multiple iterations of reanalysis through the POW may be performed without committing the changes to the database. After each reanalysis, Inspectra displays are updated to reflect any changes. Each time a sample is reanalyzed, a Differences window appears. This window summarizes the changes from the original analysis values and the last

reanalysis results. The Differences window displays these changes in a text format and includes peaks added, peaks deleted, ROIs modified, and nuclides identified in Figure 39.

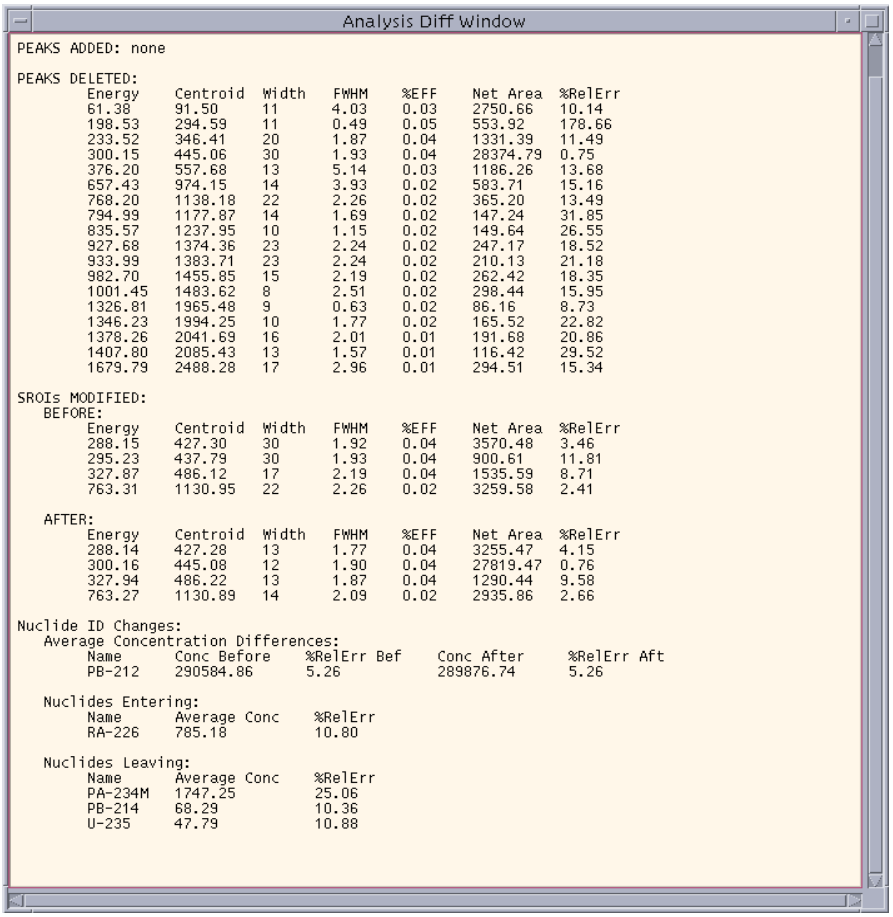


FIGURE 39. DIFFERENCES WINDOW

Once the user is satisfied with the parameter settings, the values can be committed to the database by clicking the Commit button.

Sample Release

The Sample Release window, Figure 40, provides functionality which supersedes the previous methods of releasing samples. It displays data in a summary format to be viewed prior to the release of a sample.

To access the Release Sample window, proceed as follows.

1. Choose Processing>Release Sample. The Release Sample window appears.

   The summary data provided is as currently found in the Categorization Nuclide Summary table on the Categorization window from the Reports pull-down on the main Inspectra window menubar. In addition, it displays the Hold state of each nuclide, which can be manipulated through a toggle button on the display and set to On or Off for each nuclide. The Hold value represents a simple flag to either update (Off) the data base with the most current values or maintain (On) the existing values for the nuclide. The default value for Hold is the most current value in the **gards_sample_cat** table. When the sample is released, the **gards_cat_template** and **gards_sample_cat** tables will be updated accordingly.

2. Click Cancel.

   You are returned to the Inspectra Tool window.

The Sample Release Window also contains a summary of all the comments associated with that particular sample. These comments include those from the Sample General Comments and the Sample Peak Comments windows.

To prevent unauthorized users from releasing samples, the Sample Release Window has been tied to the MAR Tool permission check features. (A user cannot open the release window for a sample unless the sample has been assigned to that user and the user has permission to release samples.) Before sample release, a confirmation prompt appears. The user must confirm or cancel the action before proceeding further in Inspectra. For more information about the MAR Tool, see “MAR Tool Procedures” on page 119.

There are new options with regard to how a sample is released. These options are executed through push-buttons located at the bottom of the window. Descriptions of each release option are listed below.

- Release. The sample is released with categorization.
- Release w/o Cat. The sample is released without categorization.
- Mark Other. This button is available when the user has selected a Mark Other option from a pull-down list located below the Mark Other button. The pull-down list allows a sample to be marked Viewed.
- Pass to Role. This button enables the user to pass the sample on for high-level review. A role must be selected from the pull-down list below the Pass to Role button. When this option is executed, the sample will be deleted from the current user's assignment queue and passed to the new role.

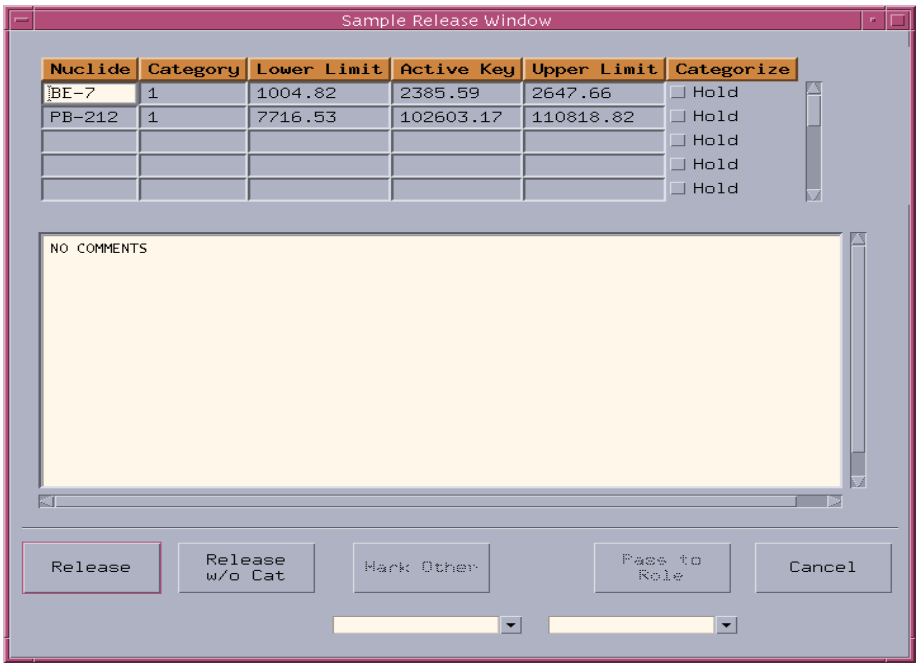


FIGURE 40. SAMPLE RELEASE WINDOW

Add General Comment

The General Comments menu selection provides a way for analysts to add additional explanation for actions taken or judgments made during the interactive analysis of a sample. General comments appear in the RRR. Just as there is a list of predefined peak comments, Inspectra will now have the ability to store predefined general comments through a new window (Figure 41). The new Add General Sample Comment Dialog operates very similarly to the peak comments window; however, it does not allow a user to insert both a user defined and predefined comment at the same time. The new Add General Sample Comment Dialog can be accessed under the "Add General Comments" pushbutton under the "Processing" menubar selection.

To add comments, proceed as follows.

1. Choose Processing>Add General Comment.

   The Add General Sample Comment Dialog appears (Figure 41).

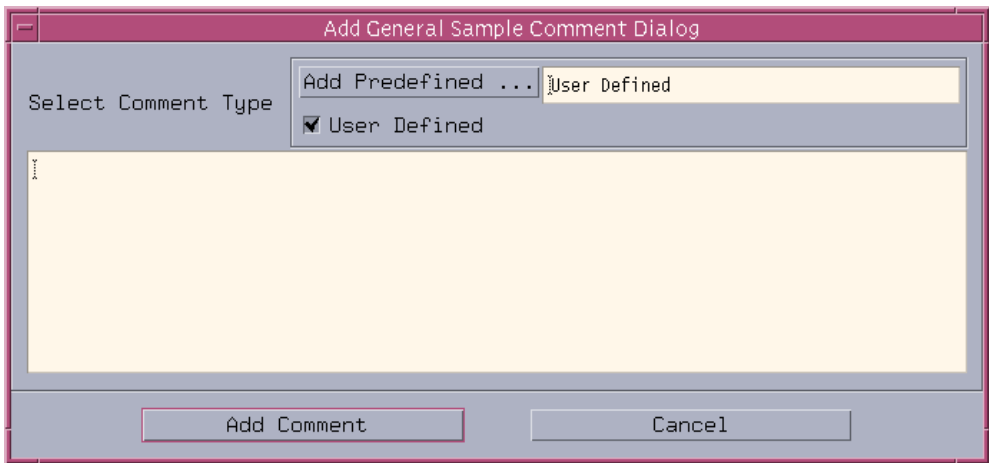


FIGURE 41. ADD GENERAL SAMPLE COMMENT DIALOG

2. Select the text box Enter General Comments to Add.
3. Enter comment(s).

4. Click OK or Apply. If you determine that no action is required, click Cancel.

   You are returned to the Inspectra Tool window.

5. Select a predefined comment using the “add predefined button” just as you would with the peak search window.

Toolbar

The Inspectra toolbar permits users to easily navigate the various capabilities of Inspectra. Horizontal and vertical versions of the toolbar are available. To display the toolbar, proceed as follows:

1. Choose the Toolbar option under the Inspectra main window menubar.

   The options `Horizontal` and `Vertical` appear.

2. Choose either a horizontal or vertical toolbar.

   The toolbar pop-up window appears, Figure 42.

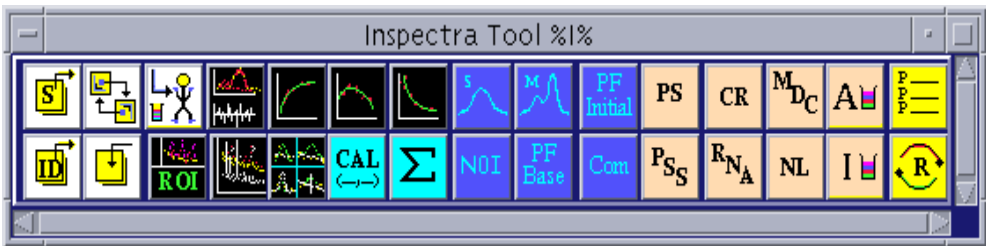


FIGURE 42. INSPECTRA HORIZONTAL TOOLBAR

The toolbar allows the user the option of opening Inspectra sub-windows without having to select them from Inspectra’s main window menubar. The face of each push-button displays a pixmap; balloon pop-ups appear when the user places the cursor over each button. These pop-ups provide a text display of the menu option that each button represents. When a button is clicked it displays the corresponding window or make modifications to a window which is currently displayed.

The toolbar is color coded in an effort to help the operator navigate to the desired functionality.

- Buttons with a white background correspond to file operation: Open Sample ID, Open Sample, Reload Sample, Close Sample and Open Sample Assignment Queue.
- Buttons with a black background open windows that provide some type of graphical display: Spectral Compare, ROI, Nuclide Review, Residual Plot, Resolution Energy Regression, Efficiency Energy Regression and Energy Channel Regression.
- Buttons with a light blue background correspond to Calibration information: Calibration Pairs and Equations.
- Buttons with the dark blue background allow toggling of values on the Spectrum Plot tab of the Configuration Dialog Window: Singlets, Multiplets, Peakfit Initial, Peakfit Baseline, NOI and Components.
- Buttons with a light brown background correspond to report information: Peak Search, Peak Search Summary, Categorization, Radionuclide Activity, Minimal Detectable Concentration, Nuclide Library, Analysis Log and User Action Log.
- Buttons with a yellow background correspond to processing options: Parameter Override and Sample Release.

Both the vertical and horizontal toolbars may be sized to display a single button or to display all buttons. In some cases, when a user clicks one of the push-buttons on the toolbar, a sample must be open in order for the chosen window to be displayed.

ILLUSTRATIVE INTERACTIVE ANALYSIS: PARTICULATE SAMPLE

These steps are representative of current procedures at the PIDC. It is assumed that the user is assigned the sample and that the sample was automatically processed without problems. It is recognized that each data center or laboratory institutes its own procedures.

1. Open the sample from the Open Sample Dialog window.
2. Check general comments and station comments.
3. Examine the Sample Detail Dialog information, including flow rate, sampling time, decay time, and acquisition time to determine if rates match expected values.
4. Compare (overlay) the MRP sample and the Preliminary sample to observe any potential energy drift or loss in detector resolution since the last spectrum was received for that station/detector combination.
5. Examine the contents of the Nuclide Review window to determine if one of the primary lines of a selected nuclide is present in the spectrum as a Type II (missed peak) error.
6. Examine the Calibration tables and plots to evaluate the state of the detector calibration and the subsequent results of the energy channel regression update (ECRU) function.
7. Display all four result summaries from the Inspectra Reports menu: Peak Search, Peak Search Summary, Radionuclide Summary, and MDC.
8. Compare key results among all four summaries for data integrity, expected rates, and values.
9. Check the Analysis Log window for any problems that may have occurred during the automatic analysis process.
10. Check for fission or activation products in the Radionuclide Activity Dialog and check the natural radionuclide concentrations (^{7}Be and ^{212}Pb).
11. Check results of the prioritization process in the Categorization Dialog to evaluate the current statistical filter state of a given nuclide.
12. Verify that the WP-224 MDCs are reasonable, with respect to the sampling/counting methodology and natural background levels.
13. Determine whether the peak search program is able to associate most spectral lines with known radionuclides using the Peak Search Summary Dialog.
14. Perform a peak search review using the Peak Search Report Dialog and the Nuclide Library Dialog. Consider the following points:

- Systematic lack of peak identifications, especially at the higher end of the spectrum, are typically due to bad ECR update and/or gain shift. This should be noted and corrected.
- Check to see if the associations are reasonable.
- Check the spectrum for Type II errors (undetected peaks) and keep a written log. The log should include review notes along with sample numbers, unknowns (not in nuclide library), and Type I and II errors.
- A relevant nuclide line may be inserted through the ROI Dialog window, if needed.

15. Look at the unidentified lines. An analyst can expect the majority of unidentified lines to be one of the following.
    - Type I error (false peak, although the peak search process determines it to be one, or
    - Poorly-defined peak with incorrect centroid energy.
16. Add comments regarding all unidentified lines and lines associated with fission products or activation nuclides.
17. Mark the sample as released with or without categorization, or pass the sample on for high-level review.

CUSTOMIZING SOFTWARE

Inspectra software can be customized via a user-friendly dialog box. This function is discussed in "Plot Action Translations (Short-cut keys)" on page 50.

Chapter 4: CORIANT Procedures

This chapter provides instructions for using the CORIANT Radionuclide software and includes the following sections:

- Overview
- Feature-specific Procedures

Chapter 4: CORIANT Procedures

OVERVIEW

The purpose of the radionuclide interactive processing system is to provide organized, relevant data in a format that can be used by analysts, scientists, processing engineers, and technical management for radionuclide monitoring purposes. The purpose of the Coincident Radiation Interactive Analysis Tool (CORIANT) is to allow analysts to review beta-gamma coincidence data. CORIANT allows the viewing of three-dimensional (3-D) histogram data, two-dimensional (2-D) beta-gated gamma spectra, 2-D gamma-gated beta spectra, and the analysis results.

FEATURE-SPECIFIC PROCEDURES

To start CORIANT, proceed as follows:

1. At the UNIX prompt, type `rms_coriant` and press the Return key.
   The ORACLE Database Connection Dialog appears.
2. Enter your username, password, and database server.
   The main CORIANT display window appears.

Spectrum Menu Selections

The selections available in the Spectrum menu are shown in Table 9. Each selection is discussed in turn.

TABLE 9: SPECTRUM MENU SELECTION

Selections	Function
Open Samples	Opens samples for use in CORIANT.
Assignment	Shows the assignment of sample IDs.

Open Samples

The Open Samples menu selection allows you to query the database by sample ID. To open a sample, proceed as follows.

1. Select Spectrum>Open Samples.

   The Open Samples dialog box appears.
2. Click Open and enter the sample ID of the spectrum you wish to view.

   The sample appears in the main CORIANT window.

If there are several samples already stored in the Open Samples dialog box, you can click on the sample ID of the spectrum you wish to open and click the Set Active button. Stored samples can be removed from the Open Samples dialog box by proceeding as follows:

1. Select Spectrum>Open Samples

   The Open Samples dialog box appears
2. Highlight the sample ID of the sample to be removed and click Remove.

   The sample is removed.

Assignment

The Assignment menu selection allows the user to select a role and open a sample assigned to that role. To open a sample:

1. Select a role by using the pull-down menu on the right.
2. Highlight the chosen sample by clicking it.
3. Click the Open button.

The Refresh button is used if the database permissions of the samples assigned to a particular role have changed. By clicking the Refresh button, the tables for each role are repopulated with the most recent set of samples assigned to each role.

Report Menu Selections

The selections available in the Report menu are shown in Table 10; each selection is discussed in turn.

TABLE 10: REPORT MENU SELECTIONS

Selections	Function
Sample Data	Displays sample informatin from the database.
Station Comments	Displays comments made by the station operator.
Gamma Graph	Displays the beta-gated gamma spectrum over the full gamma-energy span.
Beta Graph	Displays the gamma-gated beta spectrum over the full beta energy span.
Station/Dector	Displays detector information.
Roi	Displays information on predefined ROIs.
Release	Displays a release window.
Library	Displays information on the possible nuclides.
EER Graph	Displays the beta-gama coincidence efficiency of each ROI in bar chart form.
Ecr	Displays the energy to channel regression equation
Count Summary	Displays the count distribution of each ROI.
Count Compare	Compares net counts to critical level (L_c) counts.
Comments	Displays comments made during interactive reviews.
Reanalysis	Allows reanalysis of the beta-gamma samples with altered procession parameters.

Sample Data

The Sample Data menu selection displays a pop-up window box containing the Sample ID, Collect Start, Collect Stop, Acquisition Start, Acquisition Stop, Sample Collection Time, Decay Time, Acquisition Time, Quantity, and Average Flow for the active sample.

This window is identical to the bar of data underneath the CORIANT histogram window.

Station Comments

The Station Comments menu selection displays a pop-up window containing specific information from the station at which the sample was collected, including the location of the gas background PHD file and any comments from the station operator.

Gamma Graph

The Gamma Graph menu selection displays a pop-up window containing the beta-gated gamma spectrum over the full gamma energy span. Like the spectrum histogram, the gamma graph displays the energy and counts of the last clicked location.

A user may zoon in on a specific area of the gamma graph. To do this, proceed as follows:

1. Left-click and hold the desired area of the gamma graph.
2. Drag the selection box to the desired size and release the left mouse button.

   The graph is resized.
3. To zoom out, right-click the mouse.
4. Select Undo Last Zoom to undo the previous zoom or Reset Graph to restore the graph to its original state. Pushing “r” at any time will also reset the graph.

Beta Graph

The Beta Graph menu selection displays a pop-up window containing the gamma-gated beta spectrum over the full beta energy span. Like the spectrum histogram, the beta graph displays the energy and counts of the last clicked location.

To zoom in on an area of the beta graph, follow the instructions above.

Station/Detector

The Station/Detector menu selection displays a pop-up window containing the Station Code, Station Description, Station Type, Detector Code, Detector Description, and Detector Type for the sample.

Roi

The ROI menu selection displays a pop-up window containing the Gross Counts, Net Counts, Critical Level (L_c), Activity Concentration, MDC, and Beta-Gamma Coincidence Efficiency. If the user has permission, he may also use the ROI window to add nuclide comments, view general comments, display a 30-day Xe MDC graph or display a 30-day Xe Concentration graph.

To add a comment, proceed as follows:

1. Select a particular nuclide by clicking the left mouse button.
2. Right-click the nuclide to bring up a list of nuclides.
3. Select Add Comment
4. Type a comment into the text area and press the OK button.

The comment can now be viewed in the Comments menu selection where it can be modified or deleted.

At the bottom of the ROI menu is the listing of the regions of interest with corresponding check boxes. Clicking one of these check boxes will highlight the particular ROI on the CORIANT spectrum graph. Clicking the check box again will remove the highlight. The Clear button will remove all highlights.

Release

The Release menu selection (Figure 43) provides the ability to release a sample or pass it to another role. The top of the menu shows the nuclides that are to be released, their categories, and their upper and lower bounds. When released, the database is updated with

new values for the activity and the new upper and lower bounds are generated. An RRR is also automatically generated, and if the sample is categorized as Level 4 or 5, and SSREB is generated as well.

The sample can also be passed to another role. For example, an analyst can view the sample and decide that further review is necessary. By clicking Pass to Role, an analyst can pass a sample onto a different role for viewing by selecting that role and pressing teh OK button. For an explanation of roles and how they are assigned, see “MAR Tool Procedures” on page 99.

To release a role, proceed as follows:

1. Click the Release button in the middle of the window.

   The Release are in the lower left corner will light up.

2. Click Release (or Release w/o Cat) and press the OK button at the bottom of the screen.

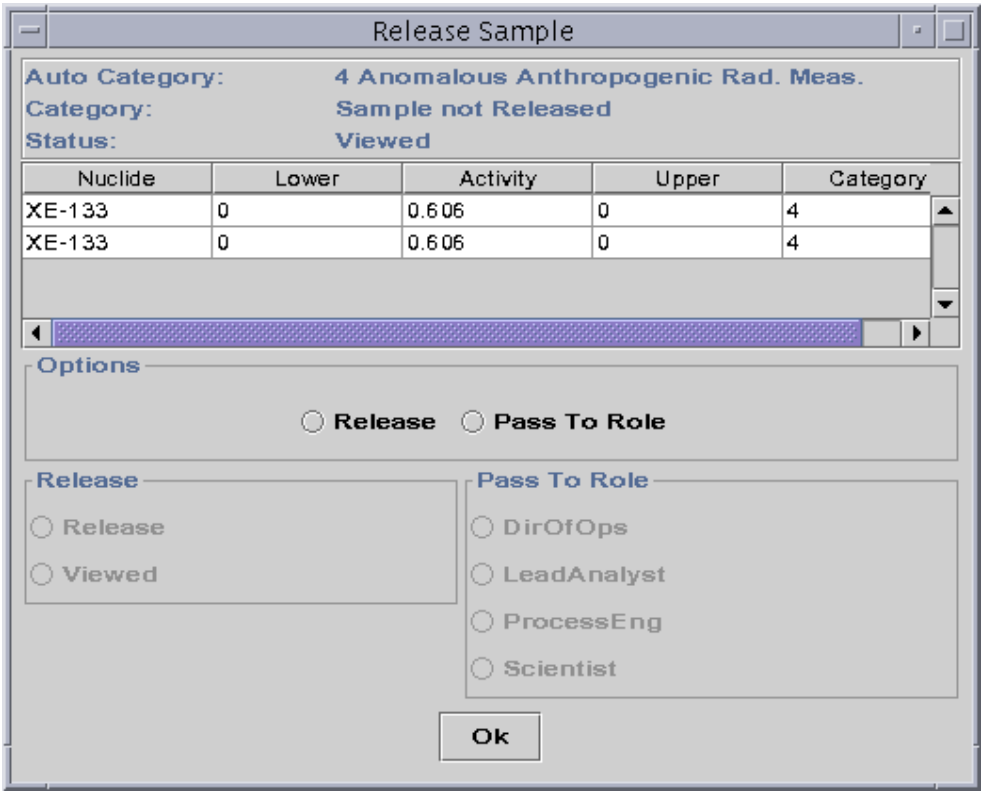


FIGURE 43. RELEASE SAMPLE WINDOW

Library

The Library menu selection displays a pop-up window listing the abundance and halflife for the nuclide of interest in each ROI.

EER Graph

The EER Graph menu selection displays a bar chart showing the beta-gamma coincidence efficiency of each ROI.

Ecr

The Ecr menu selection displays a pop-up window containing the equations used to convert channels to energy for both the gamma and beta axes.

Count Summary

The Count Summary menu selection displays a pop-up wondow summarizing the interference, memory, compton, background, and net counts of each ROI in text and pie chart formats. The text colors serve as a legend to the colors of the pie chart. The pie charts are miniatures of the charts that appear on the tabbed windows for each nuclide.

Count Compare

The Count Compare menu selection displays a pop-up window that contains net counts versus L_c in a bar chart format. The critical limit is charted in black and the net counts are charted in red.

Comments

The Comments menu selection displays a pop-up window containing analyst comments about the sample. Clicking on a comment will highlight it. Once a comment has been highlighted, clicking the Modify button will bring up a window allowing modifications. Ince the OK button is clicked on the Modifications windown, the Comments window will update automatically. If a comment is highlighted, clicking the delete button will remove it.

The Comments menu does not allow the addition of comments. To do this, the ROI menu selection must be opened, a particular nuclide row must be hightlighted, and then the analyst may right-click to add a specific or general comment. For a more detailed explanation, see the ROI Window above.

CORIANT Tabbed Windows

The main CORIANT window displays six tabbed windows. The first is the Histogram window, which shows the spectra currently under review. The other five tab windows are ROI tabs, which show detailed information about each of the possible nuclides in the sample- ^{214}Pb, ^{135}Xe, ^{133}Xe, ^{133m}Xe, and ^{131m}Xe.

Histogram Window

This Histogram window (Figure 44) shows a color-coded 2-D representation of the 3-D beta-gamma coincidence data. Each dot on the display represents the number of counts detected in one beta-gamma coincidence channel pair. The color of the dot indicates the number of counts at that beta-gamma coincidence channel.

ROI boxes can be overlaid on the histogram to highlight the five ROIs used for nuclide identification and quantification. The ROI overlay helps to determine if the energy/channel calibration equations are correct. For further explanation, refer to the ROI menu description.

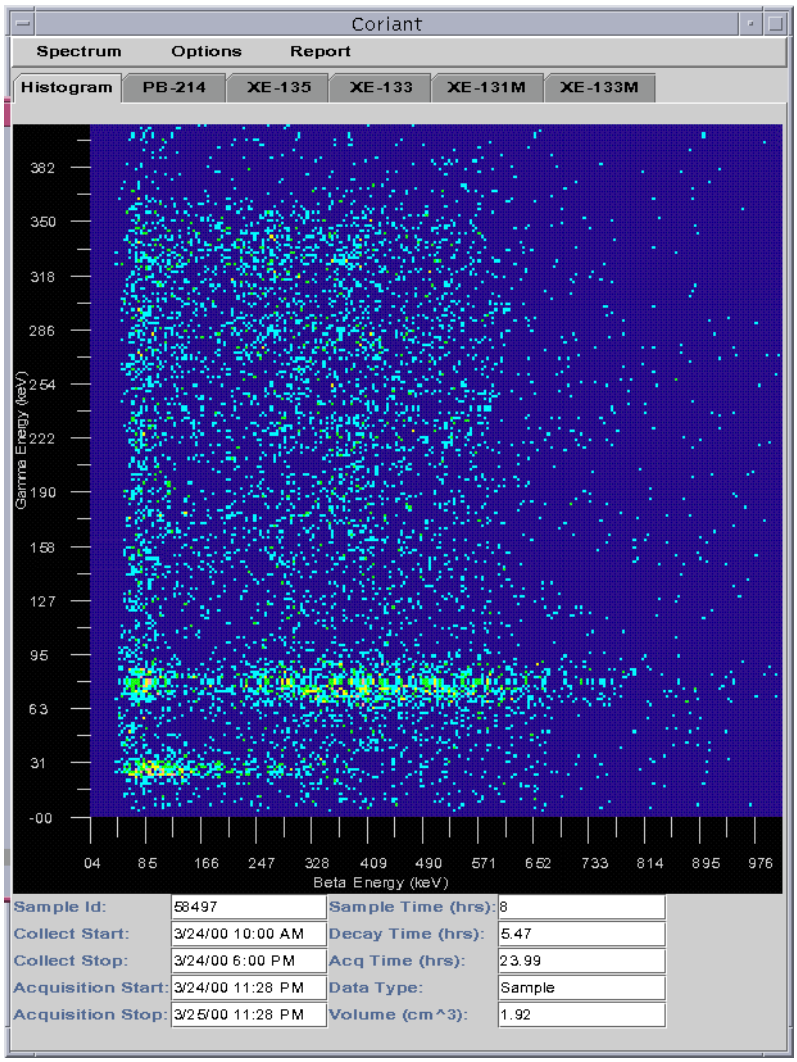


FIGURE 44. CORIANT HISTOGRAM WINDOW

It is possible to zoom in on a specific area of the Histogram tab. To do this, proceed as follows.

1. Holding down the control key, left click the mouse on the desired area of the Histogram tab.

2. Drag the selection box to the desired size and release the Control key and the left mouse button.

   The histogram is resized

3. To zoom out, press the “r” key.

   The histogram returns to the original size.

ROI Windows

Each of the five tabbed ROI windows (one of which is shown in Figure 45) represents one of the possible nuclides found in the sample. There are four sub-windows in each ROI tab.

- Beta-Gated Gamma graph - shows a plot of the beta-gated gamma spectrum over the selected ROI - zoom functionality mimics the functionality of the Beta Graph menu selection (see Beta Graph menu selection).
- Gamma-Gated Beta graph - shows a plot of the gamma-gated beta spectrum over the selected ROI - zoom functionality mimics the functionality of the Gamma graph menu selection (see Gamma graph menu selection).
- Count Summary pie chart - graphically represents how gross counts are distributed between interference counts, memory counts, Compton counts, background counts, and net counts from the automatic processing program, *rms_xanalyze*. It also lists gross count distribution in the lower left corner of the pie chart area with the colors of the text serving as a legend to the pie chart.
- Information Summary - displays three blocks of information: under Nuclide, nuclide half-life and coincidence even abundance; under Counts, gross ROI counts, net ROI counts, critical limit, and the status of the nuclide’s indentification; and under Calibration, coincident event detection efficiency, gamma energy range, and beta energy range.

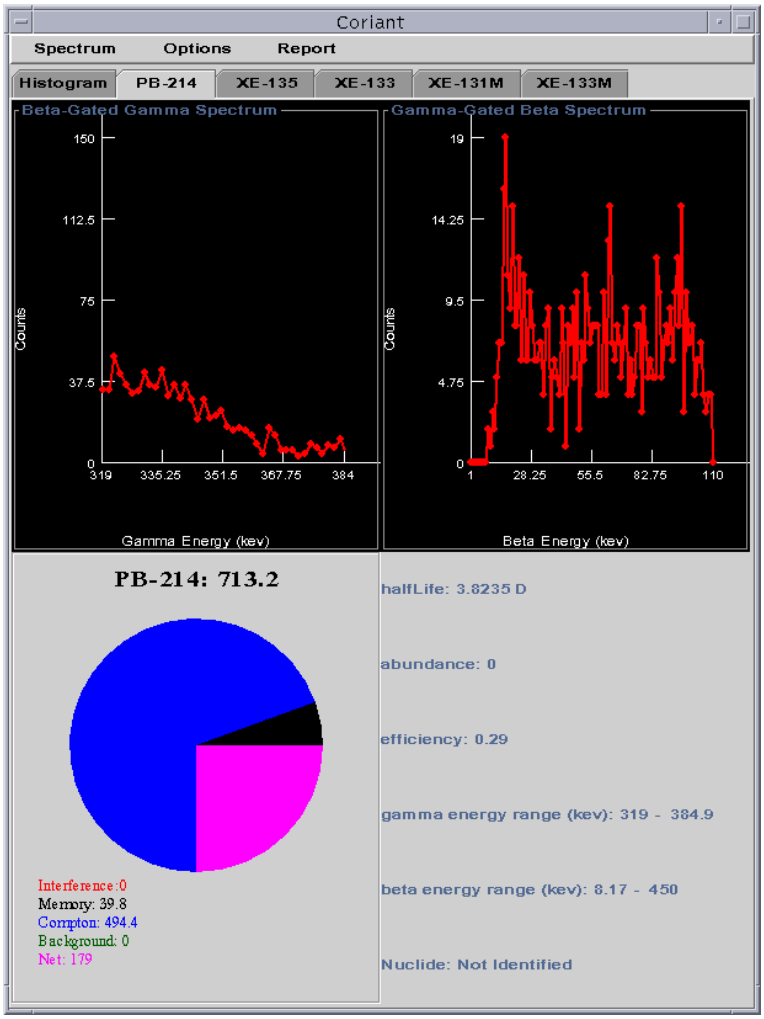


FIGURE 45. CORIANT ROI WINDOW

Chapter 5: MAR Tool Procedures

This chapter provides instructions for using the Multiple Analyst Review (MAR) Tool and includes the following sections:

- Overview
- Feature-specific Procedures

Chapter 5: MAR Tool Procedures

OVERVIEW

The purpose of the radionuclide interactive processing is to provide organized, relevant data in a format that can be used by analysts, scientists, processing engineers, and technical management for radionuclide monitoring purposes. The Multiple Analyst Review (MAR) Administrative Tool is designed to be used by a person in an administrative capacity (such as the Director of Operations) to customize the automatic distribution of samples from automatic processing for interactive review and to define which functions a user is permitted to execute while interactively reviewing samples.

FEATURE-SPECIFIC PROCEDURES

Getting Started

The MAR Tool is permissions-based and can only be executed by an authorized user. An authorized user is any user granted the MAR_admin role. To access the MAR Tool, proceed as follows:

1. At the UNIX prompt, type `rms_mar -l [login name]`
2. Press the Return key. At the prompt, enter your password.
3. The MAR Tool main window display will appear.

Main Display

The MAR Tool main display consists of four tabbed windows: Config(uration), Permissions, Roles, and Queue. The layout of each window is similar (with the exception of the Queue window); each comprises a main “Base” table on the left in the window and a secondary “Selection” table on the right. All four windows have four buttons at the bottom of the display - Commit, Modify, Reset and Exit.

Config Window

The Config window, Figure 46, displays all radionuclide stations by station code and site code. The Base table contains a list of users and the stations assigned to each user. The Selection table contains all stations that are not currently assigned to a user.

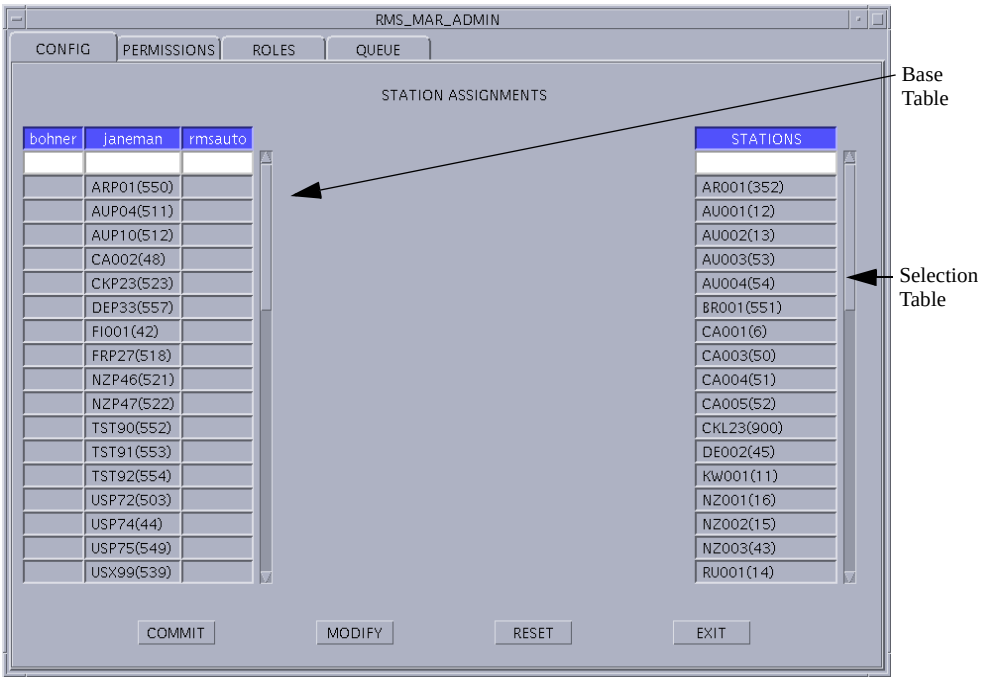


FIGURE 46. MAR TOOL CONFIGURATION WINDOW

Stations in the Selection table can be assigned to users in the Base table. Stations can also be reassigned from one user to another within the Base table. Station assignments are modified by using a drag-and-drop feature.

To assign or reassign a station, proceed as follows.

1. Click Modify at the bottom of the Config window.

   The tool's drag-and-drop feature is activated.

2. Position the cursor over the cell containing the station to be (re)assigned.
3. Click the middle mouse button and drag the station to the drop cell of the new assigned user. The drop cell is the white cell located just below the user's name in the column heading.
4. Release the mouse button.

   The station is removed from its original column and placed in the column of the new user. Both columns are resorted and the station codes are displayed alphabetically. Continue with this procedure until all reassignments are made.

5. Click Commit.

   The new assignments are saved to the database. Any new radionuclide samples that arrive in the pipeline will be assigned to users based on the new station assignment configuration.

During this process, you may choose to cancel your changes by clicking the Reset button. Clicking the Reset button reloads both tables with their original values. Once the Commit button is clicked, however, you may not reset your changes.

Permissions Window

The Permissions window, Figure 47, provides information about the specific Inspectra functions a user is allowed to execute. The functions that a user may execute are called "permissions," such as the ability to release a sample, add comments, or remove a nuclide from a spectrum. Table 11 provides a list of all the current permissions.

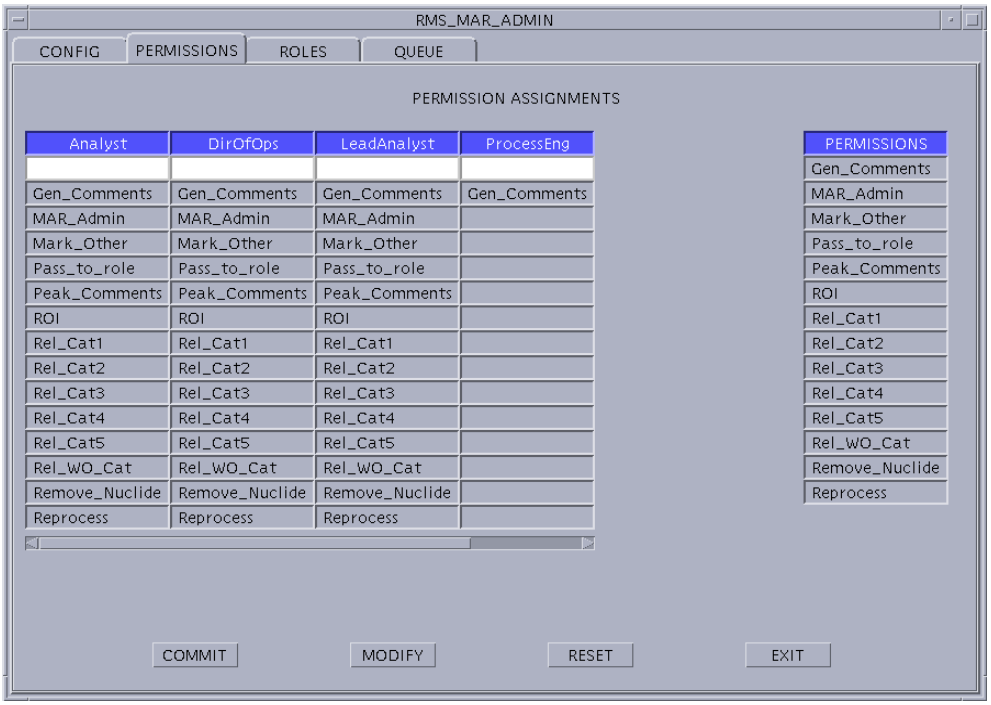


FIGURE 47. MAR TOOL PERMISSIONS WINDOW

TABLE 11: MAR TOOL PERMISSIONS

Permission	Description
Comments	Add general or peak comments during the interactive review process.
MAR_Admin	Make modifications to roles or station assignments using the MAR Tool.
Mark_Other	Mark samples as “other” during the interactive review process.
Pass_to_role	Pass a sample to another role during the interactive review process.
Rel_Cat123	Release a category 1, 2 or 3 sample.
Rel_Cat45	Release a category 4 or 5 sample.
Rel_WO_Cat	Release a sample without categorization.

TABLE 11: MAR TOOL PERMISSIONS (CONTINUED)

Permission	Description
Remove_Nuclide	Remove nuclides during the interactive review process.
Reprocess	Reprocess samples during interactive review. The user may also run *rms_analyze* from the command prompt and override default parameters.
ROI	Make changes from the ROI window during the interactive review process.

"Roles" are the various identities that a user may have, such as Analyst, Scientist, or Director of Operations. The Base table contains a list of all the roles and the permissions assigned to each role. The Selection table lists the available permissions. Table 12 provides a list of the five roles used by the MAR Tool.

TABLE 12: MAR TOOL ROLES

Role	Description
Analyst	Assigned to radionuclide analysts.
DirOfOps	Assigned to the Director of Radionuclide Operations.
LeadAnalyst	Assigned to lead analysts.
ProcessEng	Assigned to processing engineers.
Scientist	Assigned to scientists who maintain the processing parameters and nuclide libraries.

The new R3 upgrade software integrates the MAR System's roles and permissions with those in the database. Previous releases of the software did not have this capability. When a database user operating the Inspectra tool attempts to make modifications to database tables based on Inspectra actions, the database only permits the action if the appropriate database role(s) allowing the action have been granted to this user.

The coordination of the database roles and the MAR System's roles and permissions is simple. Database roles can only be modified by the user that created them. This user is called the "role owner" for the database. Depending on the schema, role owners may be

different; therefore a new database table, **gards_dbrole_owner**, was created. This table has one field specifying the database role owner. It is populated when the database is created and can only be modified by the role owner user; however, other users may be able to view it.

There is a finite list of MAR roles (Analyst, Lead Analyst, Scientist, Processing Engineer, Director of Ops) which receive default MAR permissions as a standard configuration when a database is installed. In addition, there is a finite list of MAR permissions which is contained in the **gards_permissions** table. Each MAR permission has a set of database tables that it may impact. For example, someone who is granted the MAR permission "Comments" will need "insert", "update" and "delete" permissions on the **gards_comments** and **gards_user_comments** tables. By assigning MAR permissions to MAR roles and then assigning these MAR roles to database users, a user's database write permissions will be impacted. These actions are now handled implicitly by the MAR Tool when changes of this nature are made.

To facilitate the mapping of database role names to MAR System role and permissions names a new column, *db_name,* has been added to the **gards_roles** and **gards_permissions** tables. These tables contain a list of all available MAR roles and permissions respectively. The new *db_name* field represents the database role name associated with a particular MAR role or permission. *Db_name* is used when database roles are granted or revoked as a result of a MAR role or permission change directed by the MAR Tool.

Only users with the MAR_Admin permission can run the MAR Admin Tool. Once the tool is initialized, if a user wishes to modify the assignment of MAR roles to users (Role Tab) or modify the assignment of MAR permissions to MAR roles (Permissions Tab) a new login and database reconnection is required. The login name will be that of the database role owner as extracted from the **gards_dbrole_owner** table. A prompt dialog will be displayed, requiring the login password for this user in order to proceed with the update to the database. If the password is incorrect, the update is not permitted - otherwise it is executed. After having successfully executed the command, the code reestablishes its database connection as the original user.

The assignment of database roles/permissions mirror those of the MAR System. The enhancement implementation provides a way that changes can be made interactively with the MAR Admin Tool.

There are several dependencies which need to be cared for now that the MAR System's roles and permissions are linked to the database.

Database users must be added to the MAR System. This can be accomplished by a new external script which adds the user to the **gards_user** table, sets the user's assignability flag (-1 if no roles/permissions are to be assigned to this user, 0 if no stations are going to be assigned to this user and 1 if stations are going to be assigned to this user) in this table and grants the *rms_user* database permissions. This script requires database connection as the "owner" from the **gards_dbrole_owner** table. After adding the user to the MAR System, the user will have to run the *allusers_synonyms.sql* script to make the tables visible in their local work space.

In addition, when a user is deleted from the MAR System, the *user_name* must be removed from the **gards_user** table and any references to this user's ID in the **gards_users_roles** table. All stations that are assigned to this user must be returned to an "unassigned" status and all samples assigned to the user must be reassigned to the special user "unassigned." This can be accomplish by a new external interactive script, *rms_delete_user.* The data base user's *rms_user* database permissions will be uneffected.

To assign a permission to a role within the MAR Tool, proceed as follows.

1. Click Modify.

   The drag-and-drop feature is activated.

2. Position the cursor over the cell in the Selection table containing the permission to be assigned.

3. Click the middle mouse button and drag the permission to the drop box of the role to which it will be assigned in the Base table. The drop box is the white cell located just under the role in the column heading.

4. Release the mouse button.

   The permission is added and the list is resorted and displayed alphabetically. Continue assigning permissions using this process.

5. Click Commit.

   The new permissions are saved to the database.

Permissions can be deleted from a role in the Base table by proceeding as follows.

1. Click Modify.
2. Position the cursor over the cell of the permission to be deleted in the Base table.
3. Press and hold the Control key. Click the middle mouse button.

   The permission is deleted and the remaining permissions are resorted and displayed alphabetically.
4. Click Commit.

   The changes are saved to the database.

During these processes, you may cancel your changes by clicking the Reset button. This reloads the tables with their original values. Once you have clicked Commit, you may not reset your changes. Table 13 shows the default assignment of the MAR Tool permissions.

TABLE 13: ASSIGNMENT OF MAR TOOL PERMISSIONS

Permissions	Analyst	LeadAnalyst	ProcessEng	Scientist	DirOfOps
Comments	X	X	X	X	X
MAR_Admin		X			X
Mark_Other Pass_to_Role	X	X	X	X	X
Rel_Cat123	X	X		X	X
Rel_Cat45		X		X	X
Rel_WO_Cat	X	X		X	X
Remove Nuclide	X	X		X	X
Reprocess		X	X	X	X
ROI	X	X		X	X

Roles Window

The Roles window, Figure 48, provides information on the roles assigned to various users. Users may be assigned none, one, or multiple roles with the MAR Tool. Depending on the role you have chosen while working in Inspectra or CORIANT, you may or may not have permission to execute specific functions. (See "Permissions Window" on page 122.)

Roles can be assigned, reassigned, or deleted using the same procedures as described under"Permissions Window" on page 122.

A user may have a default role. This role is identified in the **gards_users_roles** table. It provides the ability to preassign a role to a user when using Inspectra and CORIANT. This is a shortcut to selecting an identity in the Sample Assignment Queue Window of Inspectra. It also facilitates the ability to open a sample with write permission from the command line without having to first select an identity. Default roles are displayed with red text in the Role tab of the Mar Admin Tool. They can be deleted from users in the same manner as permissions are deleted from roles. A default role can be created using this tab by pressing the shift key and clicking the right mouse button down simultaneously over top of the desired role displayed in the base table of the Role Tab. To save your changes use the Commit button.

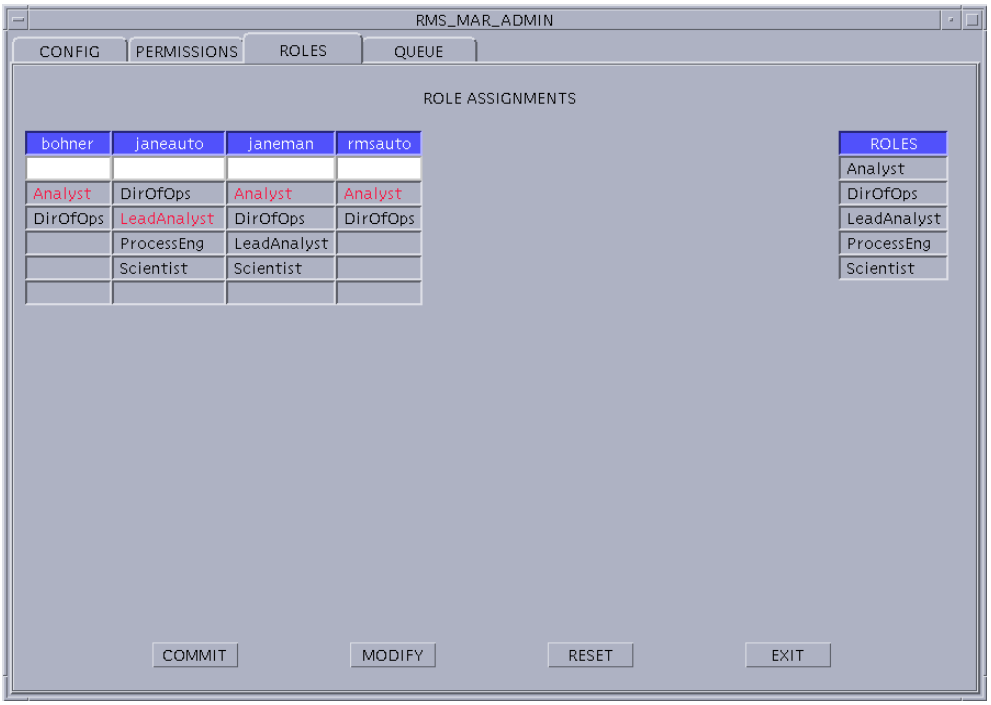


FIGURE 48. MAR TOOL ROLES WINDOW

Queue Window

The Queue window, Figure 49, is slightly different in appearance than the other tabbed windows of the MAR Tool. Instead of having a Base and Selection table, the Queue Tab has a Base table and a Static data table. The Base table is near the top of the window and contains a list of all assigned radionuclide sample IDs and the user or role to which they are assigned. Beta-gamma samples are designated with the symbol (*). The Static data table is on the bottom and lists all the assigned samples from the Base table, along with information about each sample, such as the collection stop date and the station from which the sample was transmitted. Beta-gamma samples are designated with a "_bg" on the end of the sample IDtext.

The data in each column of the Static data table can be sorted alphabetically. To do this, proceed as follows.

1. Position the cursor over the heading of the column you wish to sort.
2. Click the left mouse button. The data are sorted alphabetically.

The Queue window permits the reassignment of samples to different users or roles within the Base table. This procedure is the same as described in the Permissions Window section. Please note, there is no option to delete samples from the table, as there is in the Permissions Window and Role Window.

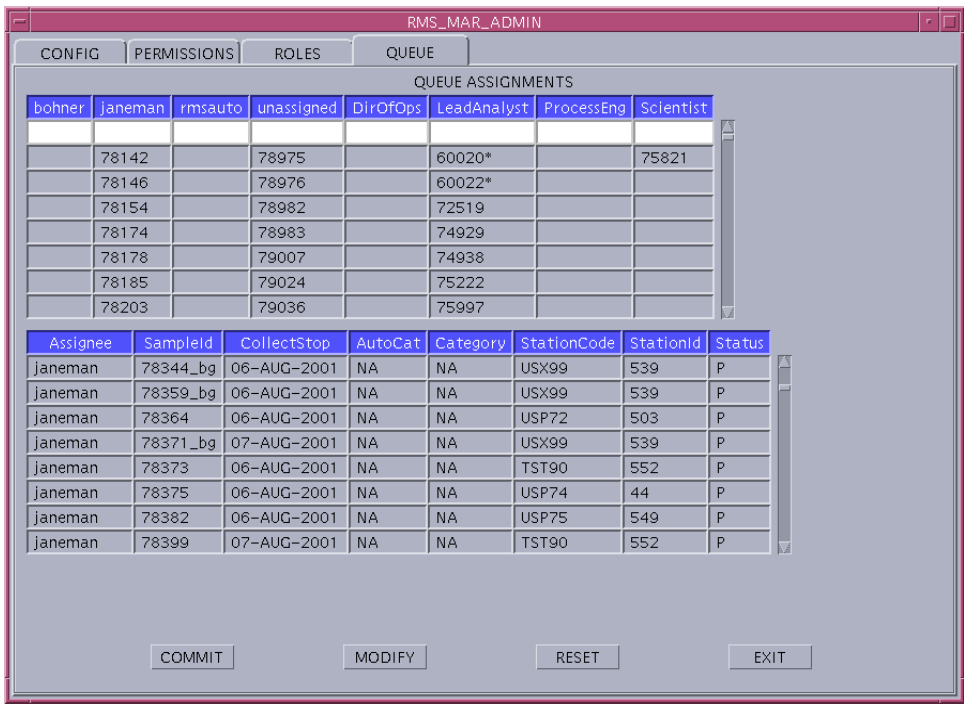


FIGURE 49. MAR TOOL QUEUE WINDOW

Frequently Asked Questions

How are the MAR System's set of roles and permissions linked to the ORACLE database's roles and table permissions?

The R3 upgrade software has linked the roles and permissions used by the MAR system with the database roles and tables permssions. Each permission available in the MAR System can potentially effect a unique set of database tables with regard to updates, selects, inserts, etc. For this reason, there are now "permissions" or database roles in the database which mirror those of the MAR tool. For example, if the MAR permission "release without cat" requires an update to the **gards_sample_status** table, any user with an MAR role holding this MAR permission must be granted this update permission in the database. This is now handled automatically by the MAR Admin Tool when roles and permissions are added/deleted or modified for users in the system.

How do you add or delete a user from the MAR System?

To add a new user, the following must occur:

1. A new ORACLE user must be created by the database administrator
2. A new interactive script, *rms_add_user*, adds this user to the MAR system. By default, this script grants a user the database role of "rmsuser." This role provides read access to all the tables. By using the MAR Admin Tool, other data base roles and table permissions can automatically be granted by assigning MAR roles to this user.
3. The script results in a new row being inserted into the **gards_users** table in the radionuclide database. The assignable field should be 1 for users who will be assigned stations and 0 for users who will not be assigned stations and -1 for users who will not be assigned roles.
4. The new user must create synonyms to the RMSMAN tables using the script provided.

To delete a user from the MAR System:

1. A new intereactive script, *rms_delete_user*, deletes this user from the MAR system. Note that the user's database login or "rmsuser" roles is not effected by this action. The action simply removes this user's association with the MAR System.
2. The above script results in a row being deleted from the **gards_users** table in the radionuclide database.

What happens when you add a new radionuclide station?

After a new station is inserted in the **gards_stations** table, a trigger inserts a record into the **gards_stations_assignment** table. The new station is assigned to the *user_id* of NULL. All of the samples received from that station will be unassigned until the station is assigned with the Config window (Figure 46 on page 121).

Will I need to create new roles and permissions?

No, the MAR roles and permisisions available with the R3 upgrade provide all of the necessary roles and permissions for the intended use of the software. They are not intented to be added to or deleted. More specifically there should be no modifications to the **gards_roles** and **gards_permissions** tables. If a modification is made to these tables, then the result will be shown in the MAR Admin Tool; however, the use of the role or permission will be superseded by database constraints since the corrolation between database permission and roles would not be linked to the MAR system permissions and roles.

Chapter 6: Trendvue Procedures

This chapter provides step-by-step instructions for using the Trendvue Radionuclide software and includes the following sections:

- Overview
- Feature-specific Procedures

Chapter 6: Trendvue Procedures

OVERVIEW

The radionuclide interactive processing system provides organized, relevant data in a format that can be used by analysts, scientists, processing engineers, and technical management for radionuclide monitoring. RMS Trendvue software provides an intuitive graphical interface for visualization of RMS data. This document provides guided instructions and interactive procedures to users of Trendvue for performing radionuclide date analyses.

FEATURE-SPECIFIC PROCEDURES

This section provides detailed instructions for using the software's features. The procedures are organized menu-by-menu and provide specific instructions for operating Trendvue software. These procedures also identify and describe Trendvue's unique window components when a graph is displayed.

Getting Started

To access Trendvue, proceed as follows.

1. At the UNIX prompt, type `rms_trendvue`
2. Press the Return key.

   The RMS Trendvue window appears as shown in Figure 50.

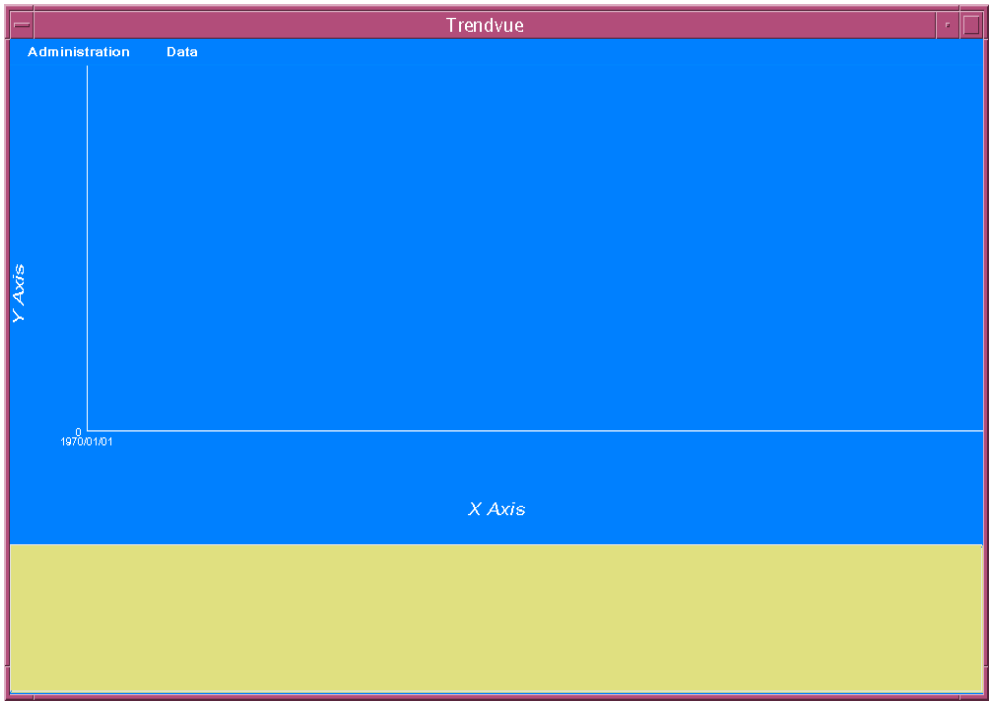


FIGURE 50. RMS TRENDVUE WINDOW

3. Under the Administration pull-down menu, select the Open Database Connection option. A Database Login window appears. Enter the appropriate information into the Username and Password boxes.
4. Click OK.

   A Message window appears indicating that the Database Connection succeeded.
5. Click OK.

Menubar

The Trendvue menubar provides Administration and Data menus. Each selection provides a submenu with a variety of capabilities as listed in Table 14.

TABLE 14: MENUBAR SELECTIONS, OPTIONS, AND FUNCTIONALITY

Menu Selection	Options	Function
Administration	Open Database Connection	Logs into the appropriate database.
	Close Database Connection	Disconnects from the appropriate database.
	Display Lines	Connects data points with lines.
	Display Points	Draws each data point as a small square.
	Display Cross-hairs	Indicates pointer location with cross hairs and displays coordinates of data points.
	Display Error Bars	Toggles error bars on/off for plots that support error bars.
	Log Plot	Toggles linear/log plot
	Date Format	Changes format of date and time
	Graph Zoom	Adjusts range of X and Y axes
	Exit	Exits Trendvue application.
Data	Add DataSet	Loads DataSet into graph panel based on user-defined options and parameters.
	View DataSet	Shows contents of the active DataSet in text format.
	Update Categori-zation Filters	Initializes categorization filters based on the active DataSet.
	Update Xe Cate-gorization Filters	Initializes xenon categorization filters based on the active DataSet
	Remove Active DataSet	Removes the specified active DataSet from the graph panel.
	View Active DataSet	Shows contents of the specified active DataSet.
	Print Active DataSet	Prints a screen shot of the graph panel.
	Remove all DataSets	Removes all DataSets from graph panel.

Trendvue Window

The Trendvue tool visually displays individual data points (based on the options and parameters set by the user), hereafter referred to as a DataSet. The graphical display of a DataSet appears in the RMS Trendvue window. Figure 51 identifies the various window components in Trendvue when a graph is displayed.

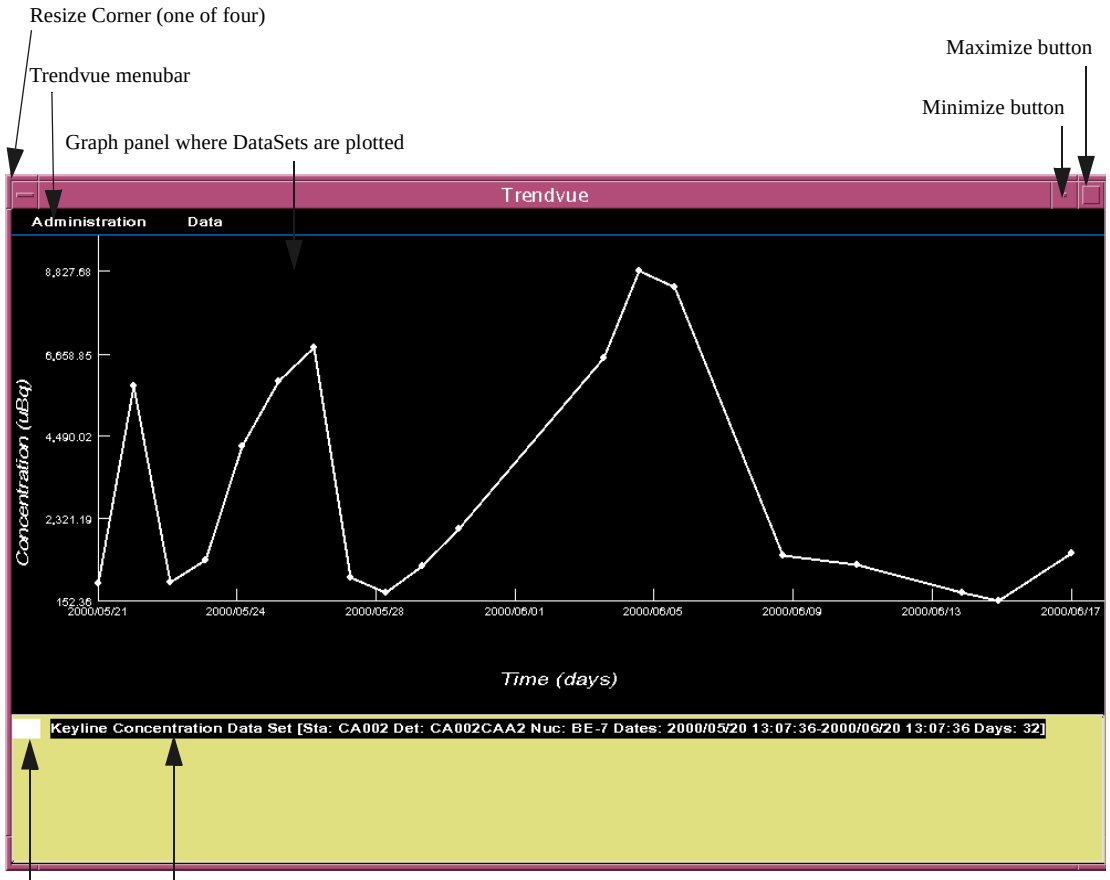


FIGURE 51. TRENDVUE WINDOW COMPONENTS

- Graph Panel

  The graph panel is the area where all graphs are plotted. The axis titles are color-coded to match the active DataSet. (The active DataSet can also be identified in the legend panel. When more than one set of data is displayed, a pressed button indicates the active DataSet.) Each DataSet is identified by one or more distinct colors.

- Display Lines

  The Display Lines option under the Administration menu controls whether the datapoints within the DataSet are connected by lines. This option is turned on by default. To turn off this option, click the Display Lines check box and all graphs will be replotted with no lines.

- Display Points

  The Display Points option under the Administration menu controls whether a small circle is drawn at each data point. This option is turned on by default. Turning this option off significantly speeds up the plot drawing for larger plots.

- Display Cross-hairs

  The Display Cross-hairs option under the Administration menu is used to control whether a cross-hair is visually displayed over a given datapoint in the chosen DataSet. This option is turned off by default. To turn on this option, click the Display Cross-hairs check box. Two new boxes will be displayed directly below the x-axis label, Figure 52.

  The cross-hair feature permits you to move from datapoint to datapoint in the graph panel. As the cross-hair is moved, the information contained in the X-Value and Y-Value boxes will automatically correspond to the indicated datapoint.

- Display Error Bars

  The Display Error Bars option under the Administration window turns error bars on and off for plots that support error bars.

- Log Plot

  The Log Plot option under the Administration menu toggles the graph between linear and log plotting mode.

- Legend

  Below the graph panel is the legend panel, which contains information about each loaded DataSet. Each DataSet is represented by a distinct color. The indicated color is used to display some or all of the datapoints within the indicated DataSet. Select an active DataSet (necessary for viewing or removing a distinct DataSet) by using the toggle button.

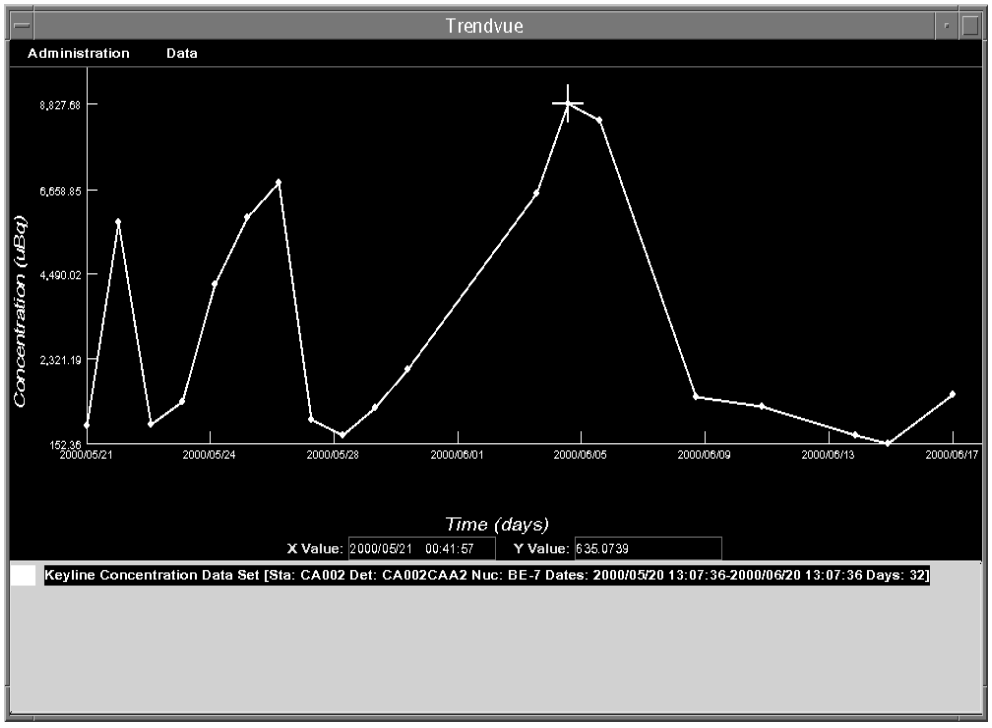


FIGURE 52. CROSS-HAIR IN GRAPH PANEL

Expanding Regions of Interest

Trendvue provides the capability to expand an ROI by enlarging the appropriate area. Instructions for exercising this ability are described below.

1. Position the mouse arrow in the graph panel on the area to be selected.
2. Press and hold the left mouse button as you move the mouse. A rectangle is drawn around the area to be expanded, Figure 53.

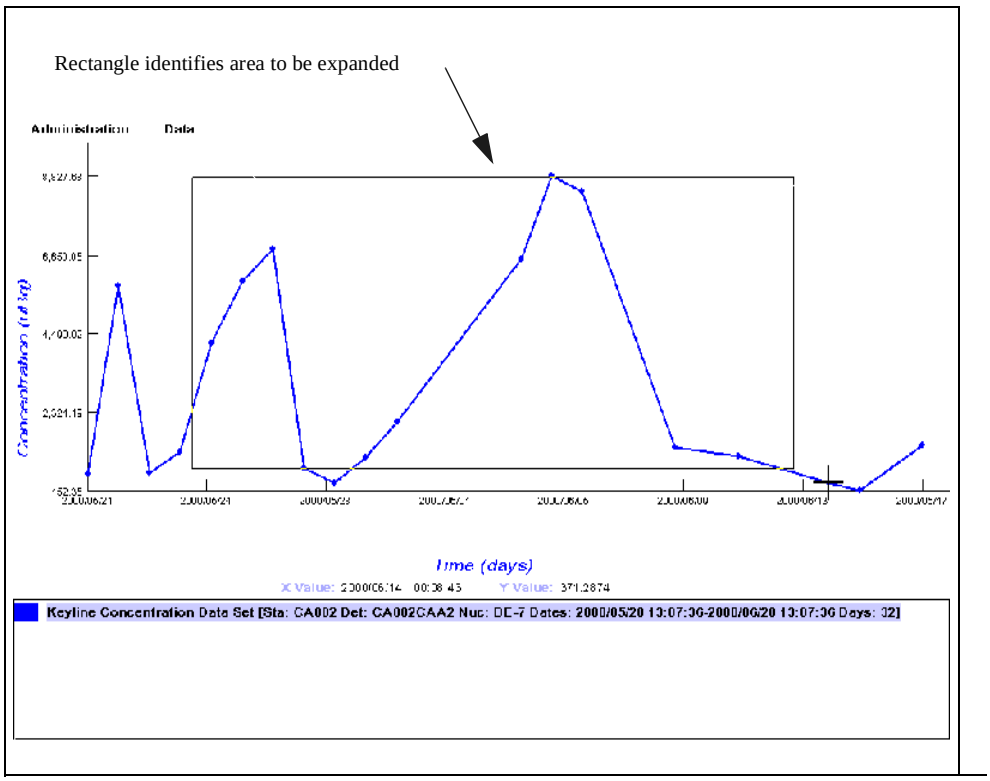


FIGURE 53. EXPANDING DATA IN GRAPH PANEL

3. Release the left mouse button to display the area in expanded mode.

4. To undo the last graph expansion or to reset the graph, click the right mouse button. A pop-up window appears with the options to Undo Last Zoom or Reset Graph. Choose the desired option and the graphical display will revert accordingly.

Menu Selections

This section provides an understanding of Trendvue's Administration and Data submenus as well as basic procedures for using submenu features. Each menubar submenu is discussed in turn.

Administration Menu Selection

The Administration menu provides data administration capabilities such as opening and closing database connections, displaying lines between datapoints, displaying cross-hairs, or exiting. Table 15 shows each Administrative submenu selection and its functionality.

TABLE 15: ADMINISTRATIVE SUBMENU SELECTIONS AND FUNCTIONALITY

Menu Selection	Function
Open Database Connection	Logs into the appropriate database.
Close Database Connection	Disconnects from the appropriate database.
Display Lines	Connects data points with lines.
Display Points	Draws each data point as a small square
Display Cross-hairs	Pointer location is indicated with cross-hairs and coordinates of data point displayed.
Display Error Bars	Toggles error bars on/off for plts that support error bars
Log Plot	Toggles linear/log plot

TABLE 15: ADMINISTRATIVE SUBMENU SELECTIONS AND FUNCTIONALITY

Menu Selection	Function
Date Format	Changes format of date and time
Graph Zoom	Adjusts range of X and Y axes
Exit	Exits Trendvue application.

Open Database Connection

You are not automatically connected to a database when logging onto Trendvue. The first option in the Administrative menu provides the capability to connect to the appropriate database. Proceed as follows.

1. Choose Administration>Open Database Connection.

   The RMS Database Login dialog box appears.
2. In the User name box, enter your user name.
3. In the Password box, enter your password.
4. In the Host name box, enter the appropriate database name.
5. Click OK.

   A Message dialog box appears, indicating that the database connection succeeded.
6. Click OK.

   The previous database connection closes and you are connected to the database as specified in the RMS Database Login dialog box. To exit the RMS Trendvue window without making any changes, click Cancel.

Close Database Connection

Choosing Administration>Close Database Connection disconnects you from the current database. No warning or confirmation dialog boxes will appear.

Display Lines

Choosing Administration>Display Lines allows you to choose whether datapoints are displayed as individual points or are connected together by a line.

With this option turned on, it may be easier to determine trends in the historical data. The default setting for this option is ON. To turn off this option, click the Display Lines check box.

Display Points

Choosing Administration>Display Points allows you to choose whether datapoints are displayed with a box as a marker.

With this option turned on, it may be easier to see the data, but for larger plots the graph redraw will be considerably slower. The default setting for this option is ON. To turn off this option, click the Display Points check box.

Display Cross-hairs

Choosing Administration>Display Cross-hairs allows the identification of an individual data point with cross-hairs. When the datapoint is selected, an X Value and Y Value box appears directly below the x-axis label. These boxes specify the values associated with the given datapoint, which are based on the options selected for graphical display.

The default setting for this option is OFF. To turn on this option, click the Display Cross-hairs check box.

Display Error Bars

Choosing Administration>Display Error Bars allows you to choose whether datapoints have error bars displayed.

The default setting for this option is OFF. To turn on this option, click the Display Error Bars check box.

Log Plot

Choosing Administration>Log Plot allows you to choose whether the plot window displays the data in linear or log mode.

The default setting for this option is OFF. To turn on this option, click the Log Plot check box.

Date Format

Choosing Administration>Date Format opens a dialog box that allows the user to specify the display format of the X-axis date. There are two radio button boxes that can be selected independently, one for date and one for time format. Two checkboxes at the top of the dialog box allow the user to turn the data or time display off.

Graph Zoom

Choosing Administration>Graph Zoom opens a dialog box that allows the user to see the current boundries of the axes. Zooming in on the graph will update these numbers automatically. Changing one or more of the axis boundry values and pressing “Apply” will update the graph’s range.

Exit

The Exit option closes the Trendvue application.

Choose Administration>Exit Trendvue.

Data Menu Selection

Various plot types represent different RMS data and require specific preference inputs (for example, collect time, location, detector), which are collected from the user through data-specific dialog boxes. The Data menu provides the capability to add, view, remove, and save DataSets. Data submenu selections and functions are shown in Table 16.

TABLE 16: DATA SUBMENU SELECTIONS AND FUNCTIONALITY

Menu Selection	Options	Function
Add DataSet	Concentration	Loads key-line nuclide concentrations based on station, detector, and date range.
	Xe Concentration	Loads calculated radioxenon concentrations based on station, detector, and date range.
	Minimum Detectable Concentration	Loads MDCs for radionuclides enumerated in [WG195], based on station, detector, and time range,
	Xe Minimum Detectable Concentration	Loads MDCs for radioxenon isotopes enumerated in [WG195], based on station, detector, and time range,
	Station Status Data	Loads station meteorological information based on inside and outside temperature, and average pressure.
	Quality Control Data	Loads detector quality control data based on gain, location, width, net area, normalized gain and K-40 location differences.
	Categorization Filter History	Loads statistical filter data for a specific station, detector, and nuclide.
	State of Health Data	Loads electronic, detector, and station-specific state of health information.
	Wind Plot	Loads wind direction data for 360^{o} graphical display.
View DataSet	Same as Add DataSet	Displays a given DataSet in tabular format, instead of a graphical representation.
Update Categorization Filters	Set Statistical Filter Parameters	Updates categorization based on either key-line or average nuclide concentrations based on station and date range.
Update Xe Categorization Filters		Updates categorization based on beta-gamma nuclides from a station.
Remove Active DataSet		Removes active DataSet from graph panel.

TABLE 16: DATA SUBMENU SELECTIONS AND FUNCTIONALITY

Menu Selection	Options	Function
View Active DataSet		Displays the active DataSet in tabular format, instead of a graphical representation.
Print Active DataSet		Prints a copy of the graph panel.
Remove All DataSets		Removes all DataSets from graph panel.

Concentration

The Concentration option displays either the keyline activity concentration or average activity concentrations of selected nuclides, based on station, detector, and date range entries. This type of information is useful for identifying temporal variations in concentrations.

1. Choose Data>Concentration.

   The Concentration dialog box appears.

2. From the Concentration pull-down menu, select Keyline or Average.
3. Select a query from status “P” and “R” samples or just from “R.”
4. To specify beginning and ending dates, follow these steps:
   - From the pull-down menu containing months, select a month.
   - From the pull-down menu containing days, select a day.
   - From the pull-down menu containing years, select a year.
     The selected dates are displayed.
5. From the Station list, select a station using the scroll bar.
6. From the Detector list, select one of the detector options displayed using the scroll bar. Only those detectors associated with the chosen station will be displayed.

7. In the Nuclide box, select a nuclide using the scroll bar or type your selection in the textbox. When selecting a nuclide from the Nuclide list, the selection automatically appears in the Nuclide box. If a nuclide is manually entered, it must exactly match one of the entries in the nuclide library.
8. Click OK.

   An example of a concentration plot is shown in Figure 54.

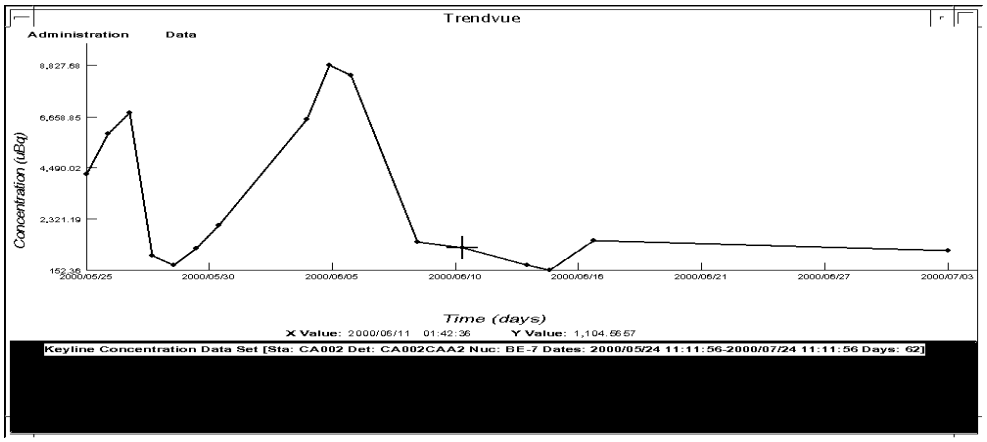


FIGURE 54. CONCENTRATION DATA

If there are no data available in the database based on the selected options, a Message box will indicate `Data Unavailable`. Click OK. You are returned to the RMS Trendvue window. To enter a new query, select Concentration from the Add DataSet menu and begin again.

Xe Concentration

The Xe Concentration option displays the keyline concentrations of selected radioxenon isotopes, based on station, detector, and time range entries. This type of information is useful for identifying temporal variations in concentrations.

To display Xe concentrations, follow the steps taken in"Concentration" on page 147. If there are no data available from the database based on the selected options, a Message box will indicate `Data Unavailable`. Click OK. You are returned to the RMS Trendvue window.

To enter a new query, select Xe Concentration from the Add DataSet menu and begin again.

Minimum Detectable Concentration

The Minimum Detectable Concentration option provides a graphical display of those nuclides enumerated in [WG195]. This type of information is useful for identifying temporal variations in MDC values.

To display the MDC values, follow the steps taken in "Concentration" on page 147. If there is no data available from the database based on the selected options, a Message box will appear indicating `Data Unavailable`. Click OK. You are returned to the RMS Trendvue window.

To enter a new query, select MDC from the Add DataSet menu and begin again.

Station Status Data

The Station Status Data option displays meteorological data (inside temperature, outside temperature, and average pressure) from a selected IMS station.

1. Choose Add DataSet>Station Status Data. Another submenu appears providing various station data selections: Inside Temperature, Outside Temperature, and Average Pressure.
2. To specify beginning and ending dates, follow the steps below:
   - From the pull-down menu containing months, select a month.
   - From the pull-down menu containing days, select a day.
   - From the pull-down menu containing years, select a year.
     The selected dates appear.
3. From the Station list, select a station using the scroll bar.

4. Click OK

   An example of the Inside Temperature plot is shown in Figure 55.

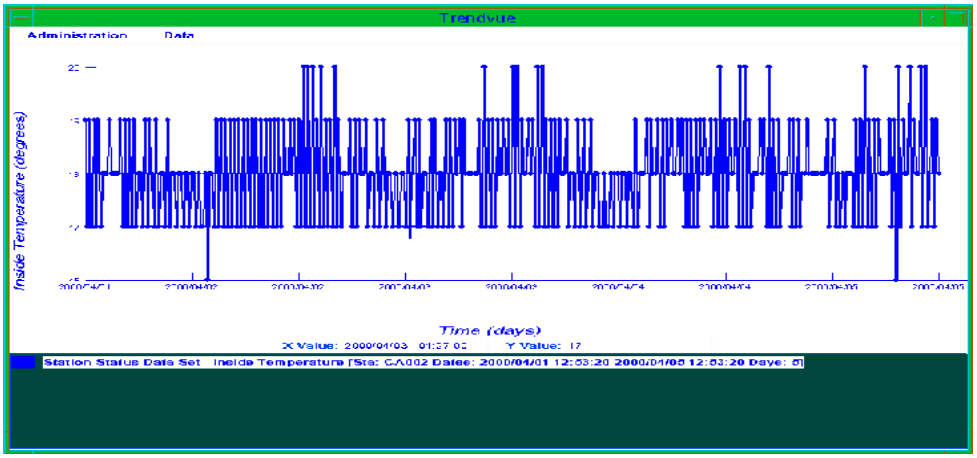


FIGURE 55. INSIDE TEMPERATURE DATA

Quality Control Data

The Quality Control (QC) option provides the ability to monitor the integrity of a given detector based on the quality control pulse height data (QCPHD) files received from a specific station. This type of information is useful in determining the state of health of a given detector over time. This may help explain poor analysis results. Specific submenu selections include normalized gain, location, width, net area, normalized gain difference, and K-40 location difference.

1. Choose Add DataSet>Quality Control Data. Another submenu appears providing various station data selections: Normalized Gain, Location, Width, Net Area, Normalized Gain Difference, and K-40 Location Difference.
2. To specify beginning and ending dates, follow these steps:
   - From the pull-down menu containing months, select a month.
   - From the pull-down menu containing days, select a day.

– From the pull-down menu containing years, select a year.
The selected dates are displayed.

3. From the Station list, select a station using the scroll bar.
4. From the Detector list, select a detector using the scroll bar.
5. A few of the submenu selections will require you to select a specific Reference Energy as well. Select one of the energies from the list provided.
6. Click OK.

An example of the Net Area plot is shown in Figure 56.

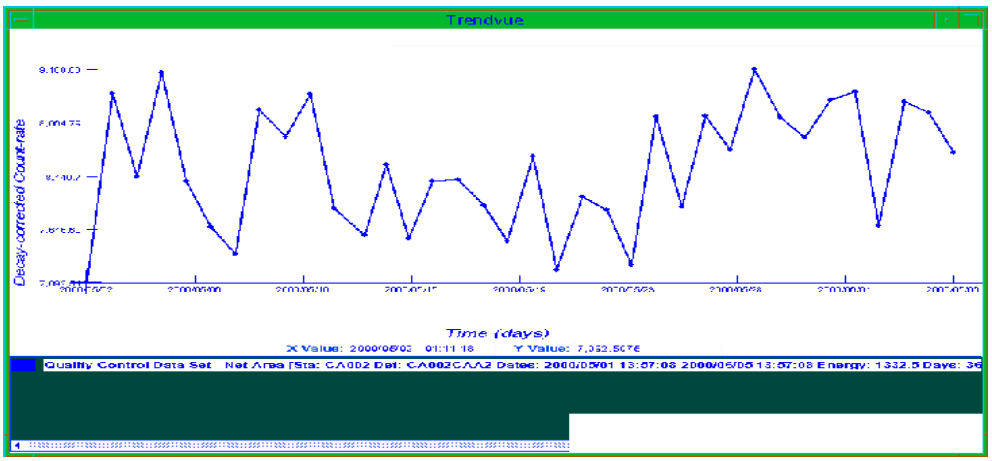


FIGURE 56. NET AREA DATA

The normalized gain plot is calculated from the centroids and energies of the highest and lowest peaks matched in the **qc_targets** database table. See [IDC5.2.2Rev2] for details on the calculation of the normalized gain.

The location plot is the centroid channels of the QCPHD for a specified reference energy, station, detector, and time period.

The width plot is the FWHM (in keV) data for a specified reference energy, station, detector, and time period.

The normalized gain difference plot indicates the difference between the calculated gain difference of one QC spectrum to its most recent QC spectrum, for the station, detector and time period selected.

The K-40 location difference indicates the change in the final channel location of the K-40 line at 1460.80 keV between consecutive samples for the station, detector, and time period selected.

The Net Area plot is the net peak area divided by *acquisition_live_sec* for the specified reference energy, station, detector, and time period. The choice of detectors consists of only those sites that send QC spectra. The choice of peak energies for display are for those nuclides found in the QC spectrum. The nuclides in these QC spectra have a known activity. The count rate is corrected for decay, therefore the plotted count rate values should be roughly constant over time.

Categorization Filter History

The Categorization Filter History option allows the display of most of the RMS categorization filter history attributes, based on station, detector, and time range entries. The plot contains the average activity of the statistical filter along with the central, upper bound, and lower bound values.

1. Choose Add DataSet>Categorization Filter History.

   The Categorization Filter History dialog box appears, Figure 57.

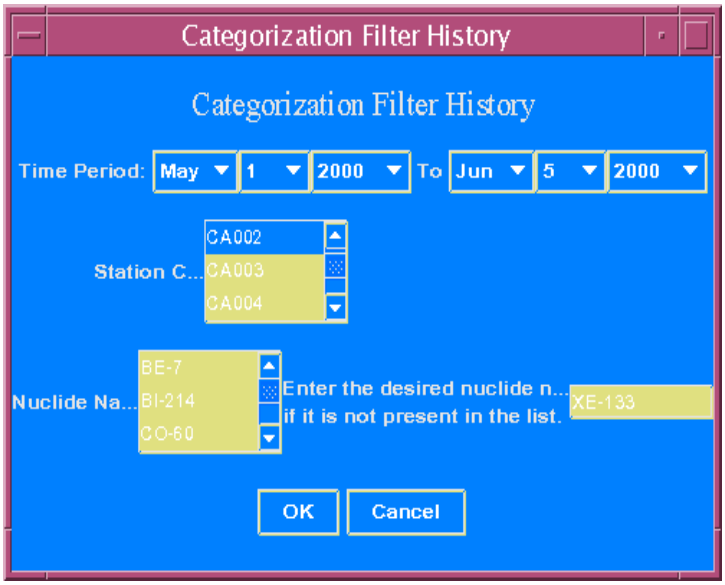


FIGURE 57. CATEGORIZATION FILTER HISTORY

2. To specify beginning and ending dates, follow these steps:
   - From the pull-down menu containing months, select a month.
   - From the pull-down menu containing days, select a day.
   - From the pull-down menu containing years, select a year.

     The selected dates appear.
3. From the Station Code list, select a station code using the scroll bar.
4. In the Nuclide box, select the nuclide desired.

   When selecting a nuclide from the Nuclide list, the selection automatically appears in the Nuclide box.
5. Click Plot DataSet.

   The data plot appears.

State of Health Data

The State of Health (SOH) option allows you to display information specific to the sample collection equipment, detector, and electronics, as well as information about the surrounding environment specific to the station, detector and time period chosen.

1. Choose Add DataSet>State of Health Data.

   Another submenu appears providing various SOH selections: Sampler Average Flow, Sampler Standard Flow, Sampler Temperature, Sampler Pressure, Room Temperature, Room Humidity, Power Supply Voltage, Crystal Temperature, Nitrogen Fill Fraction, Detector Leakage Current, and NIMBIN Voltage.

2. To specify beginning and ending dates, follow these steps:
   - From the pull-down menu containing months, select a month.
   - From the pull-down menu containing days, select a day.
   - From the pull-down menu containing years, select a year.
     The selected dates are displayed.
3. From the Station list, select a station using the scroll bar.
4. From the Detector list, select a detector.
5. Click OK.

Wind Plot

The Wind Plot option allows the display of wind directional data in a 360^{o} plot, specific to the sampler, detector, and electronics, and the surrounding environment specific to the station and time period chosen.

1. Choose Add DataSet>Wind Plot.

   Another submenu appears.

2. From the Station list, select a station using the scroll bar.
3. To specify beginning and ending dates, follow these steps.
   - From the pull-down menu containing months, select a month.
   - Enter the appropriate date for both the start date and the end date.

– From the pull-down menu containing years, select a year.
The selected dates are displayed.

4. Click Submit Query

A new window appears, providing the option to plot the wind direction by Hour, Day, Week, Month, Year, or All Period. The Print Plot button allows you to print a copy of the wind plot to either a file or a specified printer. The Normal Plot button redisplays the wind plot in a normal format, versus a zoomed-in plot, based on the highest percentage of wind direction.

An example of the Wind Direction Plot is shown in Figure 58.

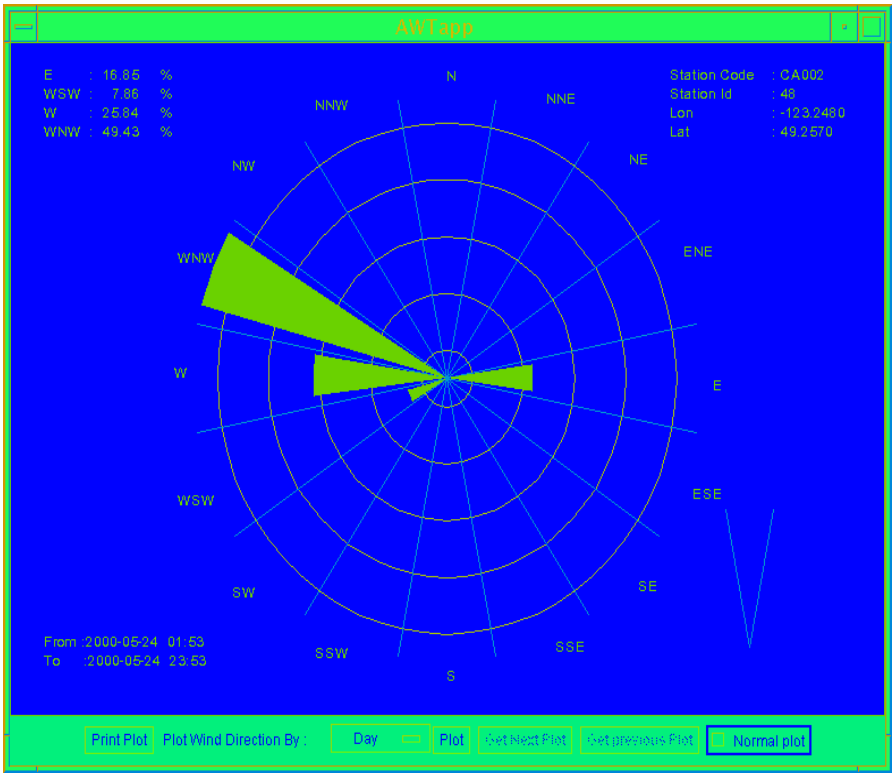


FIGURE 58. WIND DIRECTION PLOT

View DataSet

The View DataSet selection allows you to choose all of the same options available under the Add DataSet selection, except Wind Plot.

Instead of a graphical display, the DataSet Viewer provides a summary of the active DataSets in a tabular format.

1. Choose Data>View DataSet.

   The DataSet Viewer dialog box appears in Figure 59.

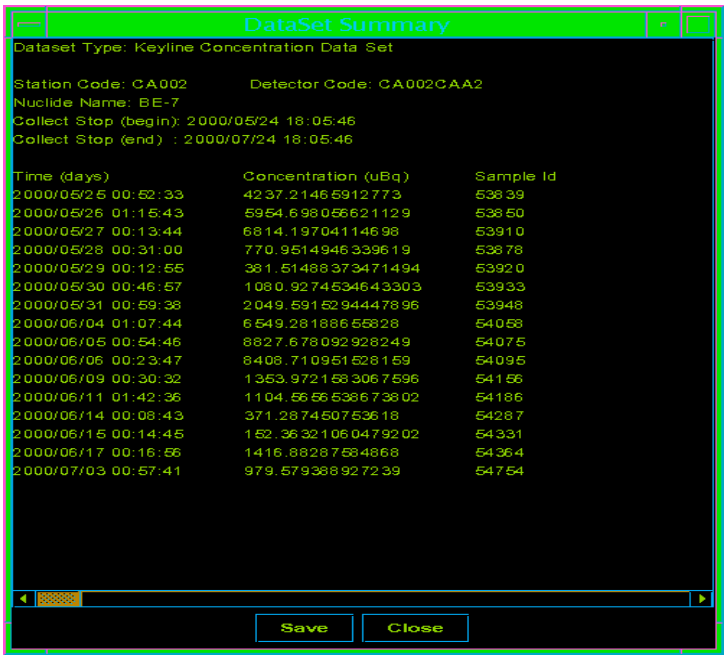


FIGURE 59. DATASET VIEWER DIALOG BOX.

2. Click the Save option to save the output to a specified file, or the Close option to return to the RMS Trendvue window.

Update Categorization Filter

The Update Categorization Filter selection provides the option to initialize or update a given categorization filter.

1. Choose Data>Update Categorization Filters.

   The Update Categorization Filter dialog box appears (Figure 60).

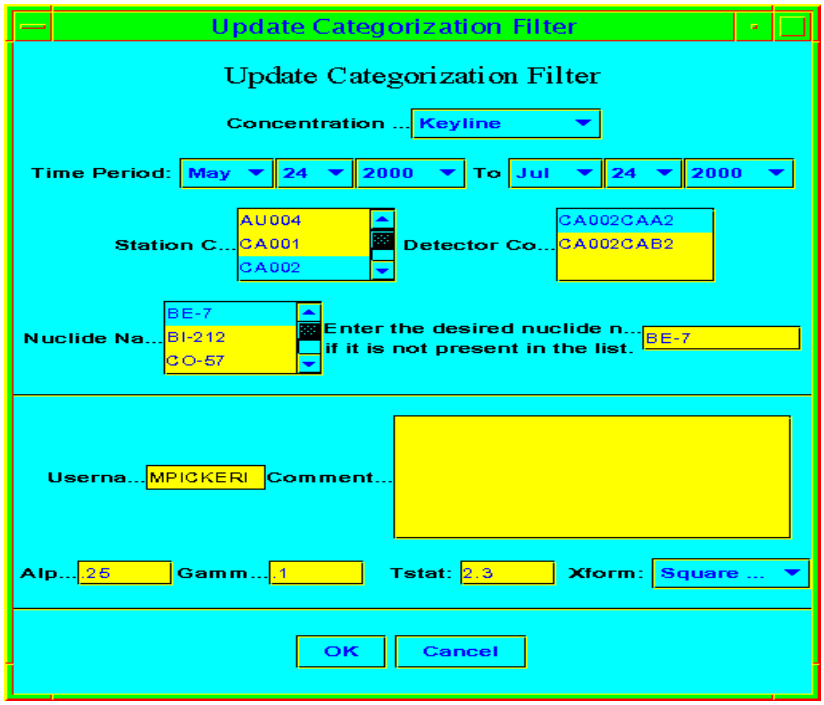


FIGURE 60. UPDATE CATEGORIZATION FILTER

2. From the Concentration pull-down menu select Keyline or Average.
3. To specify beginning and ending dates, follow these steps:
   - From the pull-down menu containing months, select a month.
   - From the pull-down menu containing days, select a day.

- From the pull-down menu containing years, select a year.
  The selected dates are displayed.

4. From the Station list, select a station using the scroll bar.
5. From the Detector list, select one of the detector options displayed. Only the detectors associated with the chosen station will be displayed.
6. In the Nuclide box, select a nuclide using the scroll bar or type an entry in the textbox. When selecting a nuclide from the Nuclide list, the selection automatically appears in the Nuclide box. If a nuclide is manually entered, it must match one of the entries in the nuclide library exactly.
7. In the Comment box, enter a comment if desired.
8. Insert the appropriate values for the Alpha, Gamma, and Tstat boxes. Nominal values for alpha, gamma, and Tstat are 0.25, 0.1, and 2.3, respectively. In addition, choose one of the Xform options from the pull-down list provided. Each selection is described below. For a more detailed explanation of these parameters see [Eva96]:
   - Alpha Gain constant for exponentially weighted moving average
   - Gamma Gain constant for variance estimator
   - Tstat statistics
   - Xform, which includes one of three forms:
     1 = Log Normal
     2 = Square root
     3 = Normal
9. Click OK to proceed with filter initialization or click Cancel to return to the RMS Trendvue window.

   If the OK button is clicked, an Update Categorization Filter window appears. This new window displays the calculated Average Activity, Delta, Lower Limit, Central Value, and Upper Limit values to be assigned to the statistical filter state.
10. Click Yes to save the categorization filter update to disk, or No to return to the RMS Trendvue window.

Remove Active DataSet

The Remove Active DataSet selection permits the removal of the active DataSet from the RMS Trendvue graphing panel. The DataSet to be removed must be active.

1. If the DataSet to be removed is not already active, then select the DataSet using the toggle button.
2. Choose Data>Remove Active DataSet.

   The active DataSet is removed from the RMS Trendvue dialog box.

View Active DataSet

The View Active DataSet selection permits you to view the active DataSet in tabular format.

1. If the DataSet to be viewed is not already active, select the DataSet using the toggle button.
2. Choose Data>View Active DataSet.

   The active DataSet is displayed in a new window in tabular format.

Print Active DataSet

The Print Active DataSet selection permits you to print a copy of the current graphing panel regardless of which DataSet is active.

1. Choose Data>Print Active DataSet.

   A new window appears to allow you to select which printer will print the image (in `.gif` format).

Remove All DataSets

The Remove All DataSets selection will allow you to remove all DataSets simultaneously.

1. Choose Data>Remove All DataSets.

   All of the DataSets are removed from the RMS Trendvue dialog box.

Chapter 7: Analyst Work Area Procedures

This chapter provides step-by-step instructions for using the Analyst Work Area Radionuclide software and includes the following sections:

- Overview
- Basic Procedures
- Feature-specific procedures
- Interactive Procedures

Chapter 7: Analyst Work Area Procedures

OVERVIEW

The purpose of the radionuclide interactive processing system is to provide organized, relevant data in a format that can be used by analysts, scientists, processing engineers, and technical management for radionuclide monitoring. The Analyst Work Area (AWA) is an intranet tool that facilitates the ability to identify and prioritize spectral data requiring review upon arrival at the IDC.

BASIC PROCEDURES

Access Control

IDC intranet access is required to access this software.

Getting Started

To access the AWA software, proceed as follows:

1. Connect to the intranet.
2. Choose the intranet address for the Analyst Work Area Map from your Web browser.

   The Analyst Work Area Network Map application window appears (Figure 61).

If you do not have the AWA Network Map bookmark properly configured, then see your System Administrator for the Uniform Resource Locator (URL).

Using Menus

All intranet browser menubar functions operate with the AWA software as with any other Web-based operation.

Using Common Commands

Common Web-based commands and short-cut keys are used with this software. AWA uses the IDC intranet browser's short-cut keys, function keys, control keys, formats, and other features for displaying its software.

Stopping/Suspending Work

The browser menubar provides stopping and suspending work capabilities, as described below.

1. To stop a process, click the Stop button from the web browser menubar.
2. To reinitialize the application page, press the Reload button.
3. To exit AWA, choose File>Exit.

   You are returned to the UNIX prompt.

FEATURE-SPECIFIC PROCEDURES

This section provides detailed instructions for using the software's features. These procedures also identify and describe AWA's unique window components and toggle buttons for viewing radionuclide data.

Understanding AWA Window Elements

The AWA application appears with three main options in the Panel Views box: Projection, Filters, and Click Functions. As a default, each function is active when accessing this software. To switch a toggle button on or off, press the toggle button and click the Redraw Map button. More than one option can be selected at a time.

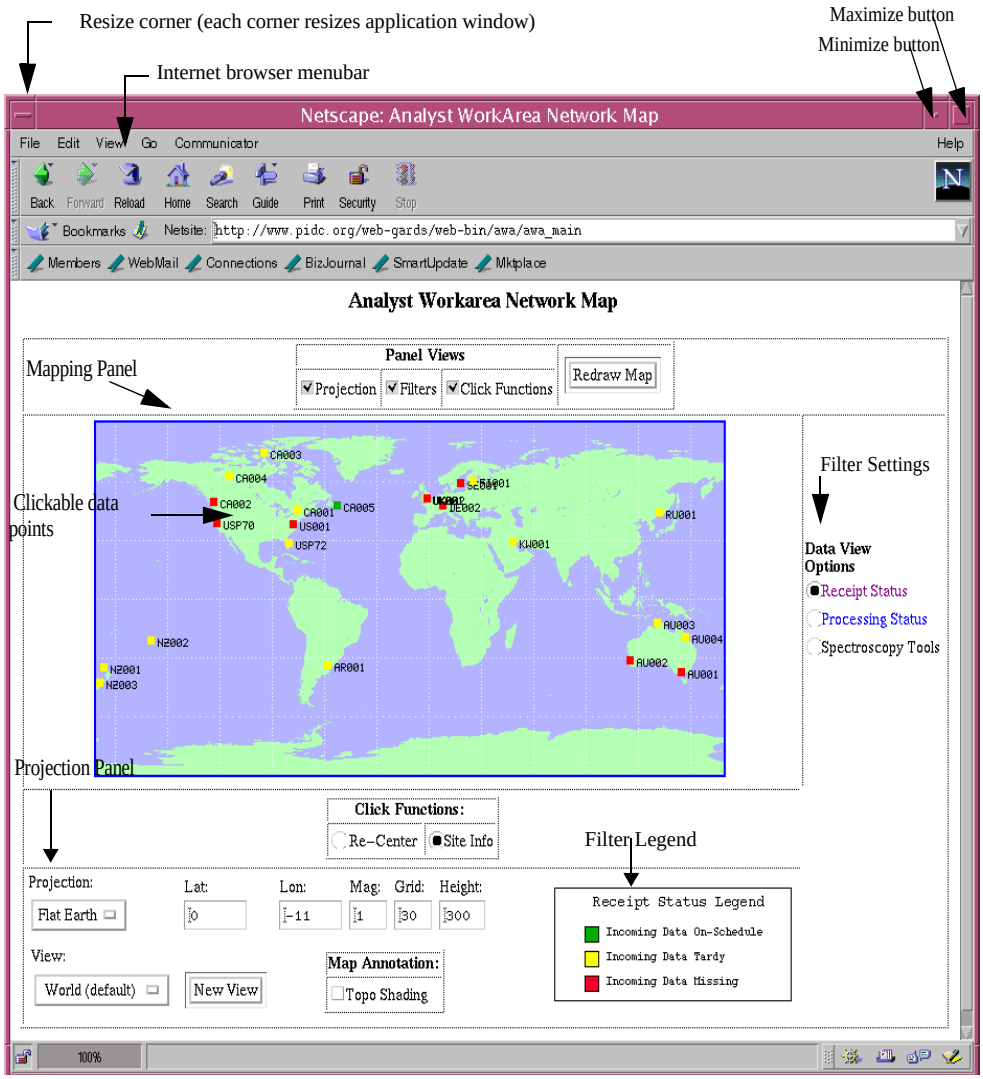


FIGURE 61. AWA WINDOW ELEMENTS

In the mapping panel, a map appears with multi-colored locator symbols. Each shape indicates the location of a station collecting radionuclide data. When clicking on a station locator symbol, a dialog box appears providing information as specified by the chosen data view options. The Filter Legend lists the meanings of the station locator symbols.

Each of the Panel View Options activates another set of options that provides specific information about the radionuclide data received at the IDC. Panel View options are described in Table 17.

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TABLE 17: PANEL VIEW OPTIONS

Option	Functions
Projection	Provides various map projection display functions along with the Filter Legend.
Filters	Provides Data View Options: Receipt Status, Processing Status, and Spectroscopy Tools.
Click Function	Provides Re-center and Site Info options.

Understanding the Projection Panel

The Projection Panel provides the ability to specify the type of map displayed, define a map perspective, and expand or zoom into a specific location on the map. The Projection Panel also provides a legend, which is discussed in greater detail in "Understanding Filter Settings" on page 168.

The Projection Panel contains a pop-up menu, text boxes, and toggle buttons. Each function is listed in Table 18 and discussed in turn.

TABLE 18: PROJECTION PANEL MENUS, BUTTONS, AND TEXT BOXES

Option	Functions
Projection	Displays an Orthographic (Ortho), Mercator, and Flat Earth projection in the mapping panel.
View	Displays a map of specific locations: World (default), Europe, and North America in the mapping panel.
Perspective	Latitude and Longitude centers a specific location in the mapping panel, Magnitude expands a projection, Grid helps identify exact locations, and Height provides a projection having a constant height and width ratio.
Map Annotation	Displays shading that provides height and depth to the map.

Displaying Map Projections and Views

In most cases, Mercator or Flat Earth projections of the world are displayed in the mapping panel to give an overview of all areas. Other settings are available and used for various types of analysis. To specify Projection and View map settings, proceed as follows:

1. Confirm the Projection button is switched on in the Panel Views. If the toggle button is not switched on, click Projection.
2. Scroll down to the Projection Panel if necessary.
3. Click the Projection button and select a map projection. The available map selections are Ortho, Mercator, or Flat Earth (default).
4. Click Redraw Map (at the top of the screen).
5. Click the View button (at the bottom of the screen) to select a World (default), European, or North American map.
6. Click New View.

   The Projection Panel New View button works only with the View pop-up menu functions and does not implement any other display functions.

Identifying Coordinates and Visual Perspectives

The Projection Panel text boxes - latitude, longitude, magnitude, grid, and height - allow the user to visually display specific areas of the world, as well as certain map perspectives. To indicate a negative number, enter a negative operator (–) before the latitude or longitude value in the text box (for example, –129). For positive values, no operator is required.

- Latitude (Lat)
  Identifies North/South coordinates in degrees; North is positive and South is negative (numeric values only).
- Longitude (Lon)
  Identifies East/West coordinates in degrees; East is positive and West is negative (numeric values only).
- Magnitude (Mag)
  Zooms into a specific Lat and Lon with an increasing magnitude factor.
- Grid
  Determines the size of each grid displayed in the mapping panel. This option is helpful as a reference point when comparing the location of one station to another.
- Height
  Indicates the height of the displayed map (projection will contain a constant height-width ratio). Increasing this value results in an increase in the size of the mapping panel.

To specify a particular map perspective, proceed as follows.

1. Click a data point of interest in the mapping panel.

   A dialog box appears, displaying a station's longitude and latitude as well as other site-specific information. For a more detailed discussion of data point dialogs, see "Understanding Filter Settings" on page 168.

2. Enter the Lat and Lon coordinates of the selected site in degrees (remember to use (–) to indicate a South or West direction).

3. Click Redraw Map.

   The map reappears, centering this location in the mapping panel.

To change your viewing perspective, proceed as follows.

1. Select Mag, Grid, and/or Height and enter desired values.
2. Click Redraw Map.

   The map reappears in the mapping panel.

Displaying a Topographical Map

The Projection Panel provides the ability to display a topographical map. To specify topographical shading, proceed as follows.

1. From the Map Annotation box, click Topo Shading.
2. Click Redraw Map.

   The annotated map appears in the mapping panel.

To display an annotated map of a specific View, proceed as follows.

1. Press View and select World (default), European, or North American.
2. Click New View.

   The map appears in the mapping panel.
3. From the Map Annotation box, click Topo Shading.

   The new annotated map appears.

Understanding Filter Settings

Data View Options provide filters that display specific types of station and radionuclide information on the map displayed in the mapping panel. The type of information provided by each selection is shown in the Filter Legend displayed in the Projection Panel. The colored symbols shown in the legend correlate with color-coded data points on the map and provide a quick, visual overview of important station and radionuclide data.

Clicking a symbol on the map displays a dialog box containing station information based on the specified filter option. Only one filter can be set at a given time. Table 19 identifies and describes the function of each available filter selection.

TABLE 19: AVAILABLE FILTER SETTINGS

Filters	Data Types	Functions
Receipt Status	Incoming Data On-Schedule (Green)	Informs analyst that spectrum data are received within the receipt schedule.
	Incoming Data Tardy (Yellow)	Informs analyst that spectrum data are past the receipt schedule, but still within the grace period.
	Incoming Data Missing (Red)	Informs analyst that spectrum data has not yet been received and are past the grace period.
Processing Status	Auto-Analysis Successful (Blue)	Informs analyst that all spectrum data was successfully processed.
	Spectra Failed in Auto-Analysis (Red)	Informs analyst that spectrum data was not successfully processed, indicating a possible problem.
Spectroscopy Tools	No Unreviewed Spectra (Blue)	Informs analyst that all spectral data for that station have been reviewed.
	Spectra Available for Review: Low Priority (Green)-Average Priority (Yellow)-High Priority (Red) Ranking	Color-coded data points notify analysts that a backlog of spectral data requiring analyst review is developing as well as the priority level of the data. Green: Spectra less than 48 hours old with category levels 1 and/or 3, or one or two unreviewed spectra with category levels 1 and/or 3. Yellow: Spectra with category Level 2, Spectra are 48-hours old or older with category levels 1 and/or 3, or 3 or more spectra with category levels 1 and/or 3 are waiting for review. Red: Spectra with category levels 4 and 5 are waiting for review (box indicates level 4 and star indicates level 5).

Filter Dialogs

The AWA software includes a clickable data point feature when displaying a Flat Earth projection in the Mapping Panel. Each data point displays an information dialog based on the filter setting in the Data View Options (Table 19). This dialog provides more detailed data and status information about the overall functioning of a station and the data it has collected. Each dialog displays generic station information, such as station code, location, latitude, and longitude. The data are also useful when displaying specific mapping perspectives by looking up a station and entering coordinates into the appropriate Projection Panel text boxes. Available filters dialogs are Receipt Status Filter, Processing Status Filter, and Spectroscopy Tools Filter. Each filter dialog is discussed in turn.

- Receipt Status Filter

  The Station Information dialog includes generic station data, data receipt schedules, and the lag-times since the receipt of each data type. In addition, there is the ability to display the last RRR and SPHD files for the last released sample from that station.

- Processing Status Filter

  The Processing Status dialog includes generic station data and a list of spectra that failed the automatic analysis process.

- Spectroscopy Tools Filter

  The Spectroscopy Tool dialog includes generic station data and a table that lists the current backlog of spectra that need to be interactively reviewed.

To specify a filter setting, proceed as follows.

1. From Panel Views, confirm that Projection, Filters, and Click Functions are switched on.
2. From Data View Options, select Receipt Status, Processing Status, or Spectroscopy Tools. (Only one selection may be active at a time.)
3. Click Redraw Map.
4. Scroll down to view the Legend.

5. Based on criticality, click a data point in the mapping panel to display a dialog detailing filter-specific information.

Understanding the Click Functions Panel

Click Functions provides the options Re-Center and Site Info. The Re-Center button is used to center a specific station in the mapping panel. Clicking the Site Info button displays station specific information as determined by the filters. (If settings described below are already set, you do not need to reset them.)

To re-center a station, proceed as follows.

1. From the Panel Views, confirm that Filters and Click Functions are selected.
2. From the Click Functions Panel, confirm that Re-Center is selected.
3. From the mapping Panel, click a data point.

   The map is redrawn centered on the data point.

To display Site Information, proceed as follows.

1. From the Panel Views, confirm that Click Functions is selected.
2. From the Click Functions, confirm that Site Info is selected.
3. From the Mapping Panel, select a data point.

   Station specific information is displayed.

INTERACTIVE PROCEDURES

These steps are illustrative of current analysis procedures used by analysts at the Prototype International Data Center (PIDC).

1. Access the AWA. All Panel Views are automatically selected and the Receipt Status filter is selected.
2. To determine a priority for reviewing monitoring stations and recently received radionuclide data, observe the mapping panel data points. Based on legend color-coding, click critical data points to review Station Information and sample data.

3. From the Data View Options, select Processing Status. Click Redraw Map.
4. Click the data point or station of interest and review the Processing Status information.
5. From the Data View Options, select Spectroscopy Tool. Click Redraw Map.
6. Based on color-coding, select the station of interest by priority.

After looking at the backlogged samples shown in the Spectroscopy Tool dialog, use the Inspectra or CORIANT software tool to look at a specific sample and perform a more detailed analysis.

Chapter 8: Data Workbench Procedures

This chapter provides step-by-step instructions for using the Data Workbench Radionuclide software and includes the following sections:

- Overview
- Feature-specific Procedures

Chapter 8: Data Workbench Procedures

OVERVIEW

The purpose of the radionuclide interactive processing system is to provide organized, relevant data in a format that can be used by analysts, scientists, processing engineers, and technical management for radionuclide monitoring purposes. The purpose of the RMS Data Workbench (DWB) software tool is to provide the capability to interact with the RMS database. This tool facilitates manual interaction using an enhanced GUI to add, delete, and modify the RMS database.

FEATURE-SPECIFIC PROCEDURES

Getting Started

The RMS DWB software can be accessed using the instructions below.

1. At the UNIX prompt, type `rms_dwb` and press the Return key.

   The DWB logon dialog box appears.
2. Enter your username and password.

   If your password does not work, see your System Administrator.
3. Click Connect.

   The main window, RMS DWB List of Forms (Figure 62), appears.

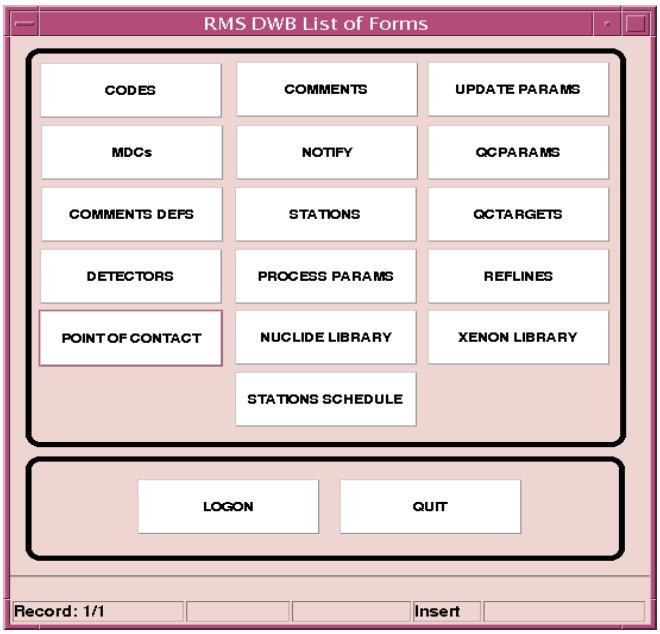

FIGURE 62. LIST OF FORMS

Form Selection

The following procedures are organized by form selection and provide specific function-by-function instructions for operating the DWB software. The LOGON selection permits you to change databases after logging into the DWB software based on permissions defined by the System Administrator for your logon.

The DWB List of Forms provides the form selections shown in Table 20.

TABLE 20: DWB FORM SELECTIONS

Form	Function
CODES	Accesses the **gards_codes** table to define, add, delete, or modify alphanumeric codes used by the RMS software.
MDCs	Accesses the **gards_mdas2report** table to add, delete, or modify the nuclide list for which MDCs will be recorded in the database and included in the RRR.
COMMENTS DEFS	Accesses the **gards_comments_defs** table to add, delete, or modify prescripted comments.
DETECTORS	Accesses the **gards_detectors** table to add, delete/archive, or modify a detector in the database.
POINT OF CONTACT	Accesses the **gards_poc** table to add, modify, or delete entries for the primary contact person assigned to each station.
COMMENTS	Accesses the **gards_comments** table to query, edit, and delete comments associated with a given spectrum.
NOTIFY	Accesses the **gards_notify** table to insert or suspend notification messages sent to personnel for special events.
STATIONS	Accesses the **gards_stations** table to add, delete/archive, or modify a station in the database.
PROCESS PARAMS	Accesses **gards_proc_params_template** table to modify parameter information used by Canberra automated analysis routines.
NUCLIDE LIBRARY	Accesses the **gards_nucl_lib** and **gards_nucl_lines_lib** tables to add, delete, or modify nuclides in the nuclide library.
STATIONS SCHEDULE	Accesses the **gards_stations_schedule** table to add or modify the data receipt and grace period schedules assigned to stations.
UPDATE PARAMS	Accesses the **gards_update_params_template** table to add or modify the parameters used during the update segment of the Canberra automated analysis routine.
QC PARAMS	Accesses the **gards_qcparams** table to modify parameters used in quality control (QC) testing.

TABLE 20: DWB FORM SELECTIONS (CONTINUED)

Form	Function
QC TARGETS	Accesses the **gards_qc_targets** table to set target widths and areas for peaks used in QC testing.
REFLINES	Accesses the **gards_detectors** table to allow for maintenance of the reference lines used in updating energy/channel relationships.
XENON LIBRARY	Accesses the **gards_nucl_lib** and **gards_nucl_lines_lib** tables to add, delete, or modify nuclides in the xenon nuclide library.

To access a form, click a particular selection. More than one form can be opened at a time.

General Form Features

Each form provides a generic menu bar: Action, Edit, Query, Block, Record, and Field. The analyst can access each of these selections using one of two methods: clicking a selection or using short-cut keys. The standard menu bar functions are described in the referenced ORACLE documentation [Bro94a].

Codes Form

The Codes Form, Figure 63, provides an interactive form to access the **gards_codes** table, which contains Type, Code, and Description information. “Type” refers to a class of code and is associated with the **gards_codes** table listed in [IDC5.1.1Rev3]. “Code” refers to actual character(s) used as identifiers in PIDC software or the database schema. The “Description” provides the meaning of a specific code. The Codes Form provides the ability to add, delete, or modify codes used in RMS software.

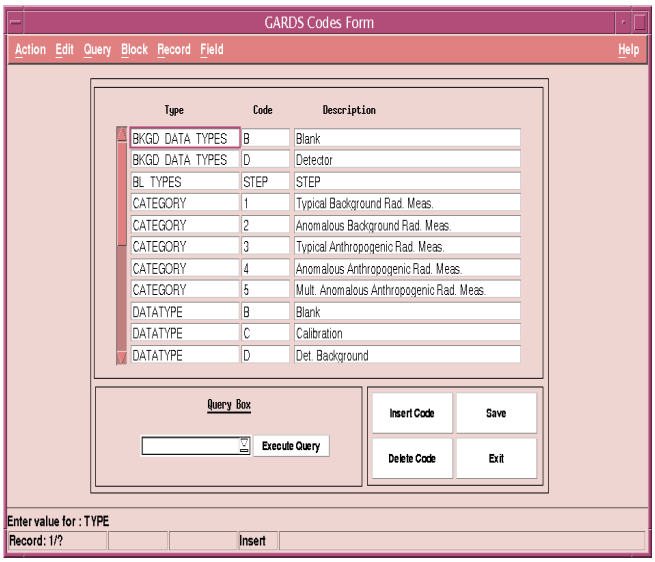

FIGURE 63. CODES FORM

Inserting a Code

To add a code to the RMS database, proceed as follows.

1. From the RMS DWB List of Forms, click CODES.

   The Codes Form appears.

2. Select Insert Code.

   The Codes Form immediately places the cursor in a blank row. Key in the appropriate information. Press the Tab key or use the mouse to move from column to column.

3. Click Save to save additions.
4. Repeat steps 2 and 3 to insert additional codes.
5. Click Exit. You are returned to the RMS DWB List of Forms window.

Deleting a Code

To delete a code form the RMS database, proceed as follows.

1. From the Codes Form, select the row containing the Type or Code you want to delete.
2. Press the Delete Code button.

   The prompt appears, "`Really delete this Code?`" with the options OK and Cancel. To delete additional codes, repeat these steps.
3. Click Save.
4. Repeat steps 2 and 3 for additional deletions.
5. Click Exit.

   You are returned to the DWB List of Forms window.

Executing a Query

To query the RMS database, proceed as follows.

1. From the Codes Form, select the text box under the Query Box heading.

   A pull-down menu appears.
2. Select one entry from the list provided and click Execute Query.

   All entries matching your query will automatically appear, along with its associated Code and Description.
3. To execute another query, repeat steps 1 and 2.
4. Click Exit.

   You are returned to the RMS DWB List of Forms window.

MDCs Form

The MDCs Form, Figure 64, provides a listing nuclides for which MDCs are displayed in the Inspectra tool and in the RRR. This form permits you to add, delete, or modify records in the list of nuclides. This form is associated with the **gards_mdas2report** table listed in [IDC5.1.1Rev3]. To access this form, proceed as follows.

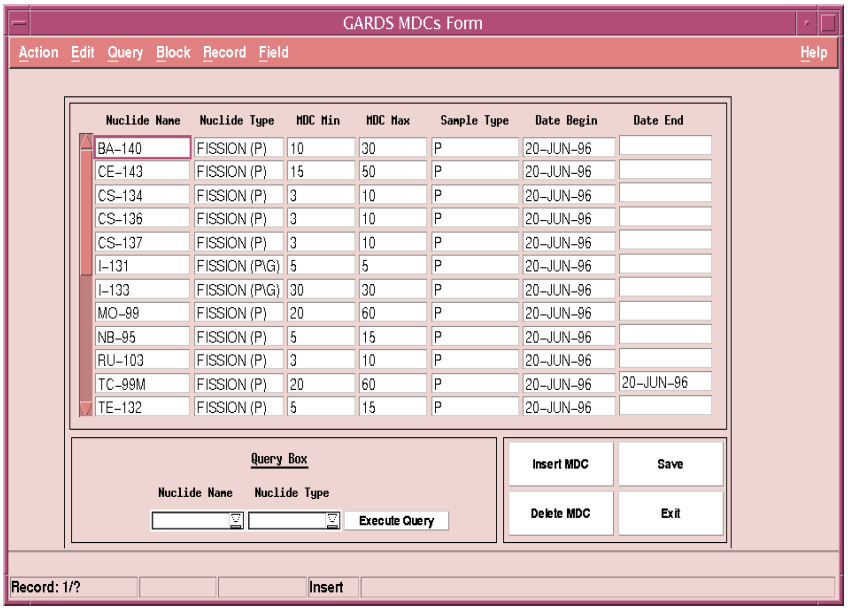

FIGURE 64. MDCS FORM

Inserting MDC Nuclides

To insert a nuclide into the RMS database (for which an MDC is to be reported), proceed as follows.

1. From the RMS DWB List of Forms, click MDCs.

   The MDCs Form appears.

2. Select the Nuclide Name column above the location where you want the new nuclide to be inserted.

3. Click Insert MDC.

   A new row appears below your selection.

4. Key in the appropriate information. Press the Tab key or use the mouse to move from column to column.

   The current date is automatically entered into the Date Begin column.

5. Select Save after each entry.

6. Click Exit.

   You are returned to the RMS DWB List of Forms window.

Modifying MDCs

To modify an existing record in the MDCs Form, proceed as follows.

1. In the MDCs Form, select the Date End column in the row containing the nuclide whose record is to be modified.

   The prompt, "`Set the date_end to current date?`" appears with the options OK and Cancel. Selecting OK automatically places the current date in the Date End column.

2. Click Insert MDC.

   A new row appears below the nuclide selected. Note: it is important to enter all modifications into a new row so that changes to the database can be tracked.

3. Enter data into each field.

   The current date is automatically inserted into the Date Begin column.

4. Click Save.
5. For additional modifications, repeat these steps.
6. Click Exit.

   You are returned to the main RMS DWB List of Forms.

Deleting MDCs

To delete an MDC, proceed as follows.

1. From the MDCs Form, select the row containing the record to be deleted and click Delete MDC.
2. Click Save.
3. For additional deletions, repeat steps 1 and 2.

4. Click Exit.

   You are returned to the RMS DWB List of Forms.

Executing a Query

To query the RMS database, proceed as follows.

1. From the MDCs Form, select one of the text boxes under the Query Box heading.

   A pull-down menu appears.

2. Select one entry from the list provided and click Execute Query.

   All entries matching your query will appear.

3. To execute another query, repeat these steps.

4. Click Exit.

   You are returned to the RMS DWB List of Forms window.

Comment Defs Form

The Comment Definitions Form, Figure 65, displays the comment type and its corresponding Comment Text. This form provides the ability to add, delete, or modify prescribed comments and is associated with the **gards_comments_defs** table in [IDC5.1.1Rev3].

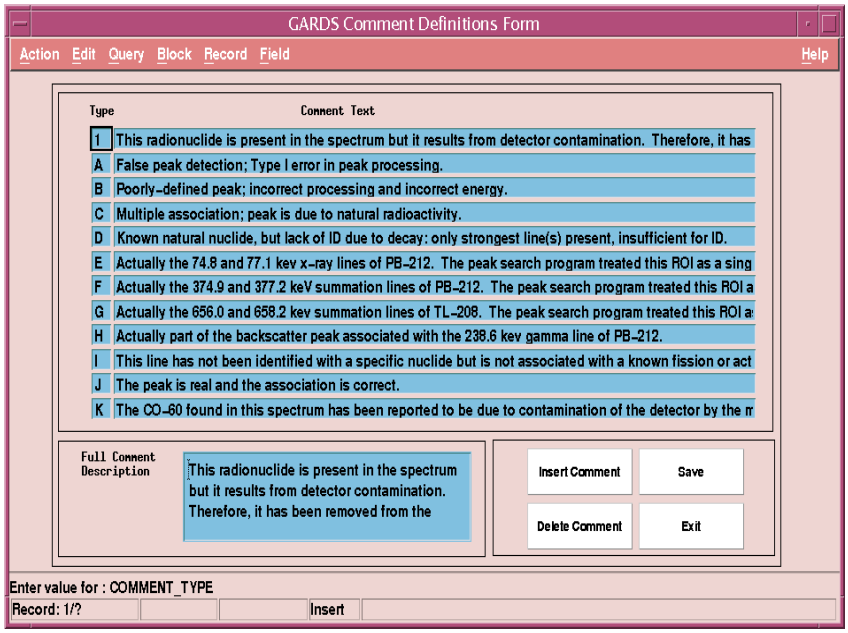

FIGURE 65. COMMENT DEFINITIONS FORM

Adding Comment Definitions

1. From the RMS DWB List of Forms, click COMMENTS DEFS.

   The Comments Definitions Form appears.

2. Select the row immediately above the chosen location for the new comment and click New Comment.

   A new row appears below your selection.

3. Select and enter data into each text box.
4. Click Save.
5. Repeat steps 2 through 4 for more additions.
6. Click Exit.

   You are returned to the DWB List of Forms window.

Modifying Comment Definitions

To modify existing comment definitions in the RMS database, proceed as follows.

1. From the Comments Definitions Form, select the Type you wish to modify.

   The comment appears in the text box.
2. Select the text box and implement changes.
3. Click Save.
4. Repeat these steps for additional modifications.
5. Click Exit.

   You are returned to the DWB List of Forms window.

Deleting Comment Definitions

To delete a comment definition in the RMS database, proceed as follows:

1. From the Comments Definitions Form, select the type you want to delete under the Type column.
2. Click Delete Comment.

   A warning prompt appears, "`There are "X number" of comments which use this comment type; delete it anyway?`" The options OK and Cancel appear.
3. Click Save.
4. Repeat these steps for additional deletions.
5. Click Exit.

   You are returned to the DWB List of Forms window.

Detectors Form

The Detectors Form, Figure 66, provides the ability to add, delete/archive, or modify a detector record in the database. This form is associated with the **gards_detectors** table in [IDC5.1.1Rev3]

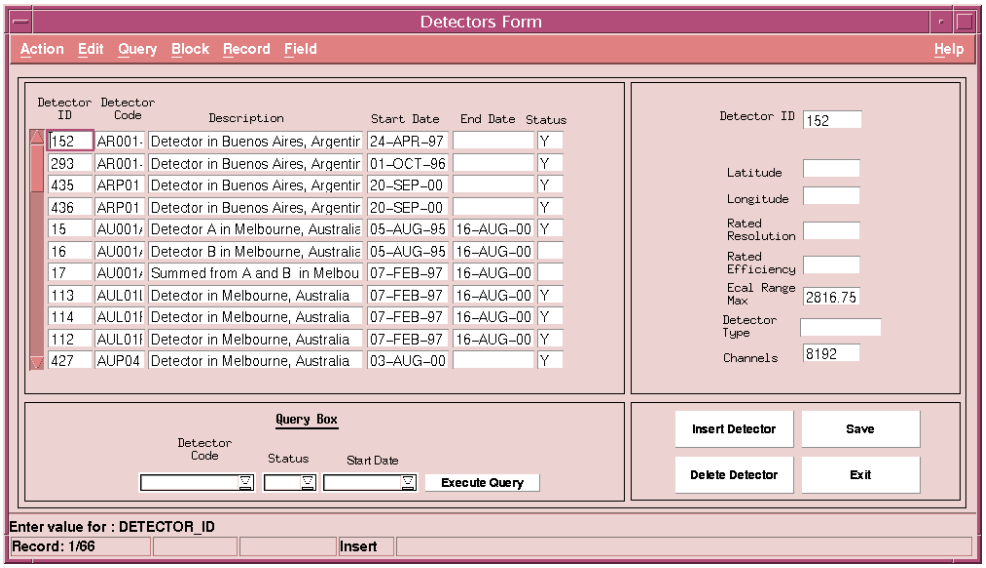

FIGURE 66. DETECTORS FORM

Adding a Detector

A detector can easily be added using the following procedure. It is not necessary to fill in all fields on this form.

1. From the RMS DWB List of Forms, click DETECTORS.

   The Detectors Form appears.

2. Click Insert Detector.

   A detector ID is automatically inserted into the Detector ID column and the current date is automatically entered into the Start Date column.

3. Select the Detector Code column and enter a valid, unique alpha-numeric code for the new detector. See [IDC3.4.1Rev2] for guidance.

4. Select the Description column and enter important information about the detector and the station location.

5. Select the Status column and type `Y` or press the Tab key to leave the column blank.

   A status of Y indicates that the detector is active and spectral data will be automatically analyzed at the Data Center upon receipt. A "blank" status column indicates that the detector is inactive and spectral data from this station will be stored unanalyzed.

6. It is not required to enter values into the remaining text boxes; however, it is advantageous to enter appropriate values for Ecal Range Max and Channels. These values may be used by the automatic analysis process during the ECR update calibration routine.

7. After all data are entered, click Save.

8. Click Exit.

   You are returned to the RMS DWB List of Forms window.

Archiving a Detector

To archive a detector, proceed as follows.

1. From the Detectors Form, select the End Date text box in the row containing the Detector ID to be archived.

   A prompt appears, "`Insert current date as date_end?`" To archive data, choose Yes. To manually enter a date, choose No.

2. Click Save.

3. Click Exit.

   You are returned to the RMS DWB List of Forms window.

Deleting a Detector

To delete a detector, proceed as follows.

1. From the Detectors Form, select the Detector ID to be deleted, and click Delete Detector.

   The row displaying that detector and all associated information is deleted.

2. Click Save.
3. For additional deletions, repeat these steps.
4. Click Exit.

   You are returned to the RMS DWB List of Forms

Executing a Query

To query the RMS database, proceed as follows:

1. From the Detectors Form, select one of the text boxes under the Query Box heading.

   A pull-down menu appears.
2. Select one entry from the list provided and click Execute Query.

   All entries matching your query will automatically appear.
3. To execute another query, repeat these steps.
4. Click Exit.

   You are returned to the RMS DWB List of Forms window.

Point of Contact Form

The Point of Contact (POC) Form, Figure 67, provides the ability to insert the primary contact person for a given station. This form permits you to add, delete, or modify the records containing POC information and is associated with the **gards_poc** table in [IDC5.1.1Rev3].

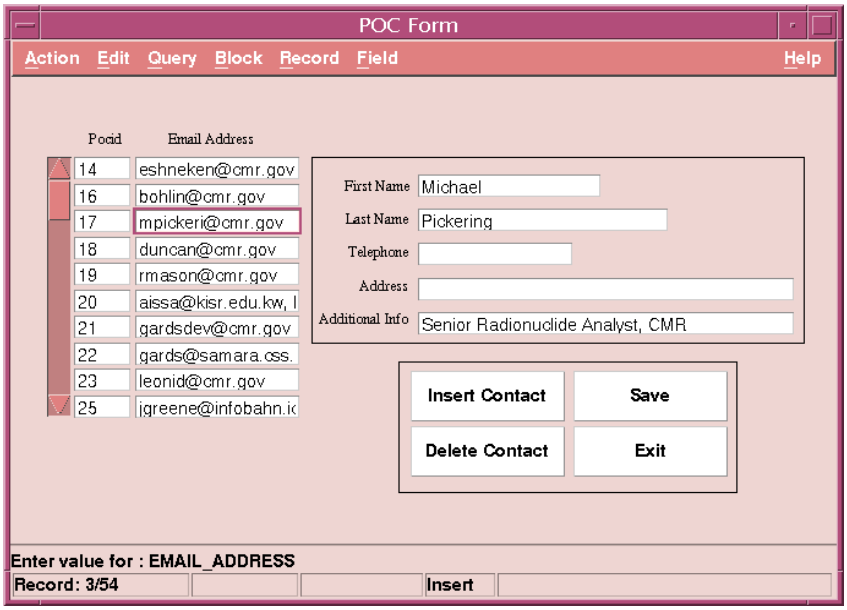

FIGURE 67. POC FORM

Inserting a POC

To add a POC to the RMS database, proceed as follows:

1. From the RMS DWB List of Forms, click Point of Contact.

   The POC Form appears.
2. Select Insert Contact.
3. A numerical value is automatically inserted into the Pocid column. Key in the appropriate information. Press the Tab key or use the mouse to move from column to column.
4. Click Save.
5. Repeat steps 2 through 4 for additional insertions.
6. Click Exit.

   You are returned to the DWB List of Forms window.

Deleting a POC

To delete a POC from the RMS database, proceed as follows:

1. From the POC Form, select the Pocid to be deleted and click Delete Contact.

   A Delete Alert prompt appears, "`Really delete this reference?`" The options OK and Cancel appear. Choose cautiously.

2. Click Save.
3. Repeat these steps for additional deletions.
4. Click Exit.

   You are returned to the DWB List of Forms window.

Comments Form

The Comments Form, Figure 68, provides the ability to query, edit, and delete comments associated with a particular sample. This form is associated with the **gards_comments, gards_comments_defs,** and **gards_user_comments** tables in [IDC5.1.1Rev3].

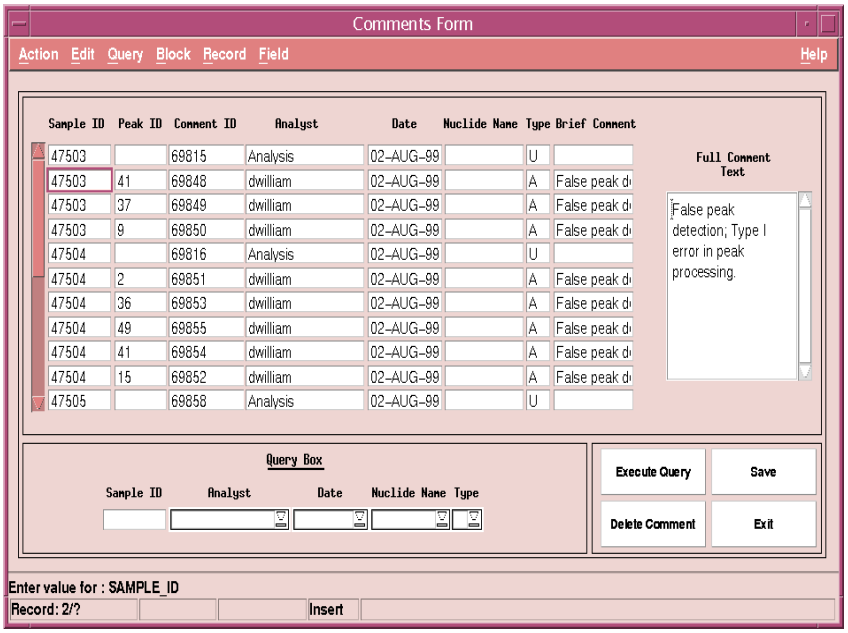

FIGURE 68. COMMENTS FORM

Editing comments

To edit existing comments in the RMS database, proceed as follows:

1. From the RMS DWB List of Forms, click COMMENTS.

   The Comments Form appears.

2. Select the Sample ID text box, key in the sample ID number to be queried, and click Execute Query.

   All comments associated with the chosen sample are displayed. The Comment ID is a unique number assigned to each comment entered via Inspectra or CORIANT. Comment searches can be narrowed by using the Analyst, Date, and Nuclide Name buttons.

3. In the Comment ID column, select the row containing the comment to be edited.

4. Select the Full Comment Text box and edit the comment. Please note that only the text of User Comments (Type 'U') can be edited. No other comment types can be modified.
5. Click Save.
6. Repeat steps 2 through 5 for additional Comment changes.
7. Click Exit.

   You are returned to the RMS DWB List of Forms window.

Deleting a Comment

To delete a comment from the RMS database, proceed as follows:

1. From the Comments Form, select the Sample ID text box, key in the sample ID number to be queried, and click Execute Query.
2. In the Comment ID column, select the row containing the comment to be deleted, and click Delete Comment.
3. Click Save.

   The prompt appears, "`Really delete this comment?`" Click Yes to delete this comment or No to terminate this deletion request.
4. Click Exit.

   You are returned to the RMS DWB List of Forms.

Notify Form

The Notify Form, Figure 69, contains event messages generated by the automatic processing routine. These notification messages are automatically sent to specific email addresses based on the following events: ALERT, NIC_SIG34, NIC_SIG5, QC_ERROR, QC_WARNING, RADOPSCAL, and RMS_ADMIN. Subscribers receive an email notification, which contains a short description of the event. The Notify Form is associated with the **gards_notify** table in [IDC5.1.1Rev3].

The ALERT, RADOPSCAL, and RMS_ADMIN messages are sent out during the input process. When an alert message is received from a station, a notification is sent to subscribers in a ALERT_TYPE message format such as ALERT_FLOW, ALERT_SYSTEM, ALERT_TEMP, and ALERT_UPS. RADOPSCAL messages are sent when new detector-specific calibration pair datasets are received at the IDC. RMS_ADMIN messages are sent when an error or unexpected result occurs during input processing.

The QC_WARNING and QC_ERROR messages are sent out during the automatic analysis process. QC_WARNING messages are sent when prescribed QC tests fail on a sample during the analysis process. QC_ERROR messages are sent when QC tests fail to complete during the analysis process.

The NIC_SIG34 and NIC_SIG5 messages are sent out during the automatic sample prioritization process. NIC_SIG34 messages are sent when a sample is prioritized as a level 3 or 4. In addition, NIC_SIG34 messages are sent out for prioritization of level 5 samples because they contain level 4 nuclides. NIC_SIG5 messages are sent when a priority 5 sample results from the prioritization process.

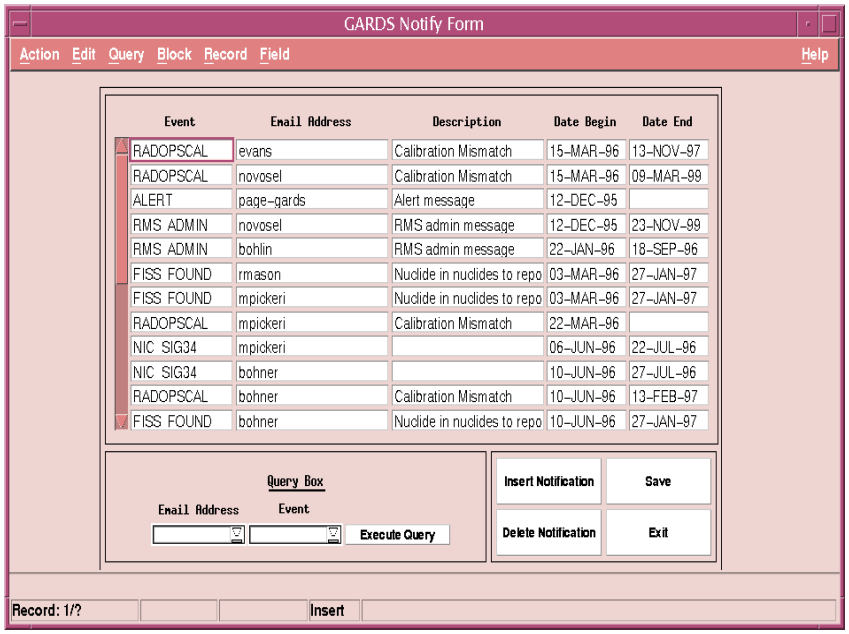

FIGURE 69. NOTIFY FORM

Inserting Notifications

To insert a subscriber into the RMS database, proceed as follows:

1. From the RMS DWB List of Forms, click NOTIFY.

   The Notify Form appears.

2. Select the row immediately above the location for the new row and click Insert Notification.

   A new row appears below the row selected. The current date automatically appears in the Date Begin column.

3. Enter data into each column. Use the Tab key or the mouse to move among columns.

4. Click Save.

5. Repeat steps 2 through 4 to insert additional subscribers.

6. Click Exit.

   You are returned to the RMS DWB List of Forms Window.

Deleting Notifications

To delete a subscriber from the Notify Form, proceed as follows.

1. From the Notify Form, select the event to be deleted and click Delete Notification.

   The prompt appears, "`Really delete record?`" Click OK to delete the event record or Cancel to exit without deletion.
2. Click Save.
3. Repeat these steps for additional subscription deletions.
4. Click Exit.

   You are returned to the RMS DWB List of Forms window.

Executing a Query

To query the RMS database, proceed as follows.

1. From the Notify Form, select one of the text boxes under the Query Box heading.

   A pull-down menu appears.
2. Select an entry from the Email Address and/or Event text box from the lists provided.

   All entries matching your query will automatically appear.
3. To execute another query, repeat these steps.
4. Click Exit.

   You are returned to the RMS DWB List of Forms window.

Stations Form

The Stations Form, Figure 70, provides the ability to add, delete/archive, or modify a station in the database. This form is associated with the **gards_stations** table in [IDC5.1.1Rev3].

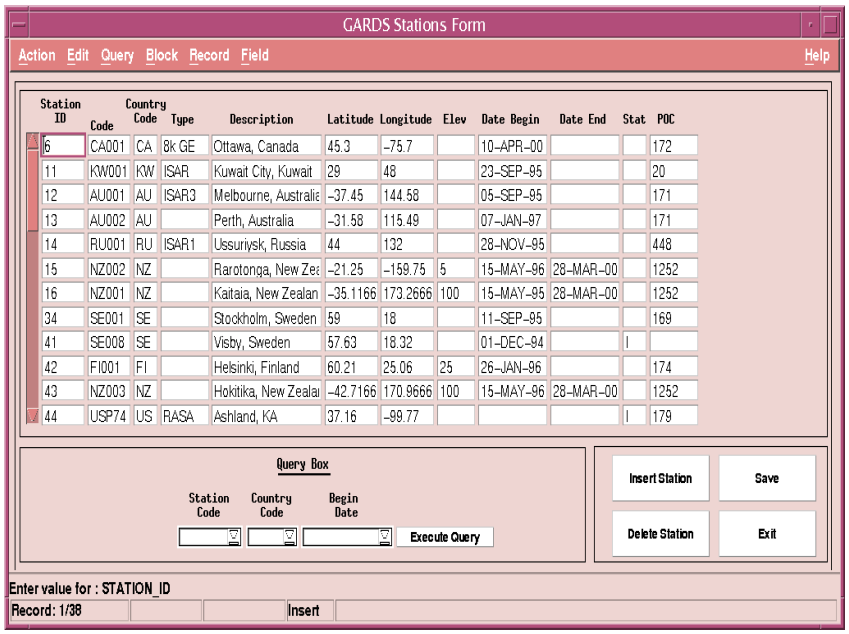

FIGURE 70. STATIONS FORM

Adding Stations

To add a station to the RMS database, proceed as follows.

1. From the RMS DWB List of Forms, click STATIONS.

   The Stations Form appears.

2. Click Insert Station.

   A distinct numerical value is automatically inserted into the Station ID column and the current date is automatically entered into the Date Begin column.

3. Select the next column, Code, and enter a valid, unique alpha-numeric code for the new station. See [IDC3.4.1Rev2]for guidance on acceptable station codes.
4. Enter data into each column. Use the Tab key or the mouse to move among columns.

   If the Date End column is accidentally selected, the prompt, "`Insert current date into date_end?`" appears. Choose Cancel to end this request.
5. Click Save.
6. Repeat steps 2 through 5 to add additional stations.
7. Click Exit.

   You are returned to the RMS DWB List of Forms.

Archiving or Deleting a Station

To archive or delete a station, proceed as follows.

1. From the Stations Form, select the Station ID to be archived and click in the Date End column.

   The prompt, "`Insert current date into date_end?`" appears. Selecting OK enters the current date and selecting Cancel ends the request.
2. Select the Station ID to be deleted and click Delete Station.

   The prompt, "`Really delete this station?`" appears. Select OK to delete the row displaying that station and associated information. Select Cancel to end this request.
3. Click Save.
4. Repeat these steps to archive or delete more stations.
5. Click Exit.

   You are returned to the RMS DWB List of Forms.

Executing a Query

To query the RMS database, proceed as follows.

1. From the Stations Form, select a text box under the Query Box heading.

   A pull-down menu appears.

2. Select an entry from the Station Code, Country Code and/or Begin Date text boxes and click Execute Query.

   All entries matching your query will automatically appear.

3. To execute another query, repeat these steps.

4. Click Exit.

   You are returned to the RMS DWB List of Forms window.

Process Parameters Form

The Processing Parameters Form, Figure 71, provides the ability to change specific parameter information utilized by the Canberra processing software in its peak identification and nuclide association routines. This form is associated with the **gards_proc_params_template** table in [IDC5.1.1Rev3].

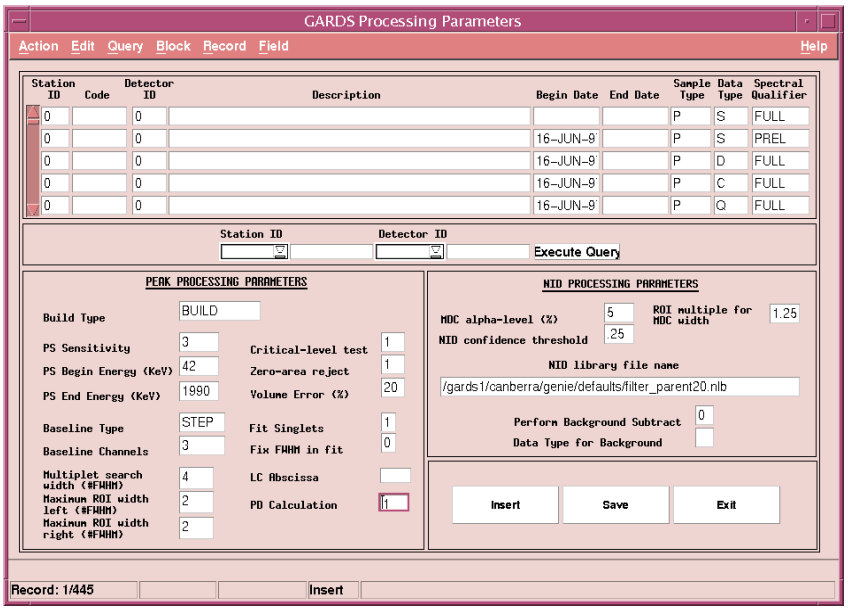

FIGURE 71. PROCESSING PARAMETERS FORM

Note that spectra from each station/detector combination are analyzed according to unique processing parameters.

Inserting or Modifying Parameters

1. From the RMS DWB List of Forms, click PROCESS PARAMS.

   The Processing Parameters Form appears.

2. Click Insert.

   The prompt, "`Do you wish to add an end date to the current record?`" appears, with the options Yes or No. If you are planning to modify the current parameters assigned to a specific station/detector entry, choose Yes, so that an analyst is able to track all changes made to the processing parameters. The current date will be inserted into the indicated record. The No option should only be selected if the new record is for an entirely new station/detector combination.

3. The prompt, "`You must enter a detector and station ID for the new record. Do you wish to copy default data to the remaining entries?`" appears. Choosing Yes copies all the current form parameters into the new record except for the Data Type, Spectral Qualifier, Build Type, and PD Calculation fields. Parameters must be inserted into these fields manually. Choosing No will leave all parameter fields blank.
4. Enter the specific Station ID and Detector ID entries to be assigned to the new record.

   If these entries match existing station and detector IDs in the RMS database, the data associated with this detector/pair will be automatically loaded into the Code and Description fields. If the Station ID or the Detector ID do not match any existing records in the database, you must manually input the code and description information. The current date is automatically inserted into the Begin Date field.
5. Use the Tab key or the mouse to move among columns, inserting the appropriate processing parameters where indicated.
6. Click Save.
7. Repeat steps 2 through 6 to add additional stations.
8. Click Exit.

   You are returned to the RMS DWB List of Forms.

Nuclide Libraries Form

The Nuclide Libraries Form, Figure 72, provides the ability to modify gamma lines; write database library information to a special nuclide library file (xxxx.nlb); and insert, modify, or delete a particular nuclide from the particulate database library. The nuclide library file is required by the Canberra software routines. This form is associated with the **gards_nucl_lib** and **gards_nucl_lines_lib** tables, in [IDC5.1.1Rev3].

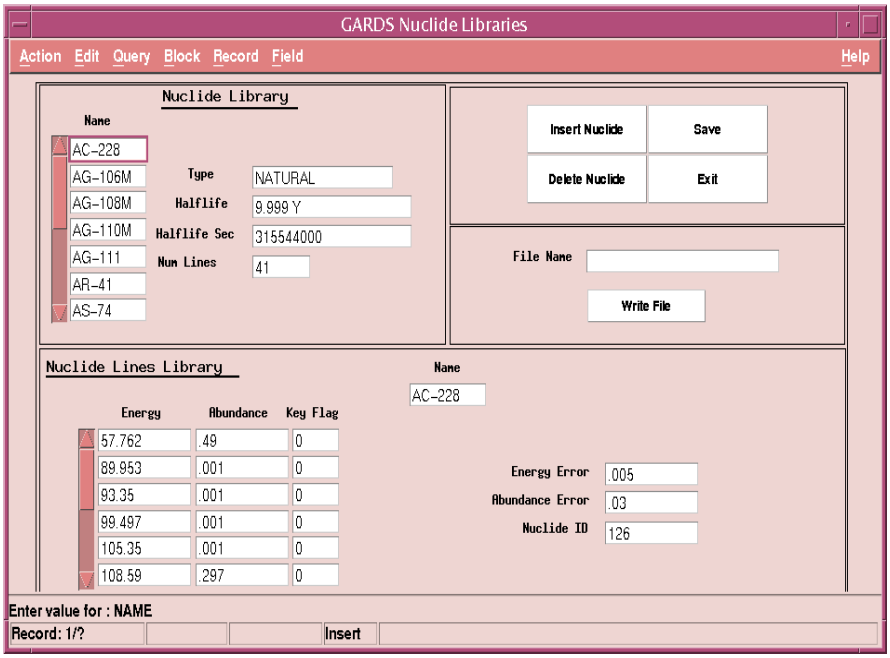

FIGURE 72. NUCLIDE LIBRARIES FORM

Adding a Nuclide

To add a nuclide to the Nuclide Library, proceed as follows.

1. From the RMS DWB List of Forms, click NUCLIDE LIBRARY.

   The GARDS Nuclide Libraries Form appears.

2. Click Insert Nuclide.

   A new row appears in the Name field. Enter the nuclide to be added.

3. Press the Tab key to move to other data fields and enter the new Type, Halflife, and Halflife Sec into the appropriate text boxes. The Num Lines entry is based on the number of lines associated with the given nuclide.

4. Click Save.

5. Repeat these steps to add additional nuclides to the nuclide library.

6. After the nuclide library is configured, write the information to an external nuclide library file (`xxxx.nlb`). The automated processing uses unique `.nlb` files for each station/detector combination. The location of the file is specified in the Processing Parameters Form in the field "NID library file name."
7. Click Exit.

   You are returned to the RMS DWB List of Forms window.

Modifying a Nuclide

To modify a nuclide in the RMS database, proceed as follows.

1. From the Nuclide Libraries Form, select the desired nuclide in the Name field to be modified. Press the Tab key to move to the data field(s) requiring modification.
2. Select the appropriate box and enter your changes. Continue until all modifications have been made.
3. Click Save.

   After the nuclide library is configured, write the information to an external nuclide library file by keying in a file name (`xxxx.nlb`). The automated processing uses unique `.nlb` files for each station/detector combination. The location of the file is specified in the Processing Parameters Form in the field "NID library file name."
4. Select the File Name text box and enter a new file name.
5. Click Write File.
6. Click Exit.

   You are returned to the RMS DWB List of Forms window.

Deleting a Nuclide

To delete a nuclide from the RMS database, proceed as follows.

1. In the Nuclide Name field of the Nuclide Libraries Form, select the nuclide to be deleted.

2. Click Delete Nuclide.
3. Click Save.
4. Repeat these steps to delete additional nuclides.
5. Click Exit.

   You are returned to the RMS DWB List of Forms.

Nuclide Lines Library

The Nuclide Lines Library section of the form displays the energy and abundance of all lines associated with a given nuclide in the Energy and Abundance columns. (See Figure 72.) The Key Flag column contains either a “0” or “1,” where a “1” indicates the keyline of a nuclide. The other text box entries (Energy Error, Abundance Error, and Nuclide ID) contain information associated with the nuclide-specific data.

Adding a Nuclide Line

To add a nuclide line to the nuclide library, proceed as follows.

1. In the Nuclide Library section of the Nuclide Libraries Form, select the nuclide requiring additional lines.
2. From the Nuclide Lines Library section, select an Energy box.
3. Click Insert Line.

   A blank row appears below the selected nuclide line. Enter information into each text box.
4. Click Save.

   The nuclide line is added for this nuclide in the nuclide library.
5. Repeat these steps to add additional lines.
6. Click Exit.

   You are returned to the RMS DWB List of Forms window.

Modifying a Nuclide Line

To modify a line in the nuclide library, proceed as follows:

1. In the Nuclide Library section of the Nuclide Libraries Form, select the nuclide to be modified.

   In the Nuclide Lines Library section, the selected nuclide appears in the Name box and its associated information is located into the Energy, Abundance, and Key Flag columns.

2. Select the Energy to be modified.

   This activates the other text boxes in the Nuclide Lines Library and displays the related information.

3. To change any nuclide line information in the Nuclide Lines Library section, select the appropriate text box and enter the data.

4. Click Save.

   The nuclide line is modified in the nuclide library.

5. Repeat these steps to add additional lines.

6. Click Exit.

   You are returned to the RMS DWB List of Forms window.

Deleting a Nuclide Line

1. In the Nuclide Library section of the Nuclide Lines Library, select the nuclide whose line is to be deleted.

2. From the Nuclide Lines Library, select the Energy box containing the line to be deleted.

3. Click Delete Line.

   The selected energy line is removed.

4. Click Save.

   This line is removed from this nuclide in the nuclide library.

5. Repeat these steps to remove additional lines.

6. Click Exit.

   You are returned to the RMS DWB List of Forms window.

Writing Library Information to a File

Information in the nuclide library can be saved to a postscript file as follows.

1. After making changes to the nuclide library, enter a file name (including the specific path) in the File Name box.
2. Click Write File.

   A postscript file is created.

Stations Schedule Form

The Stations Schedule Form, Figure 73, provides the ability to add, delete/archive, or modify a station's receipt and grace period schedule in the database. This form is associated with the **gards_stations** and **gards_stations_schedule** table in [IDC5.1.1Rev3].

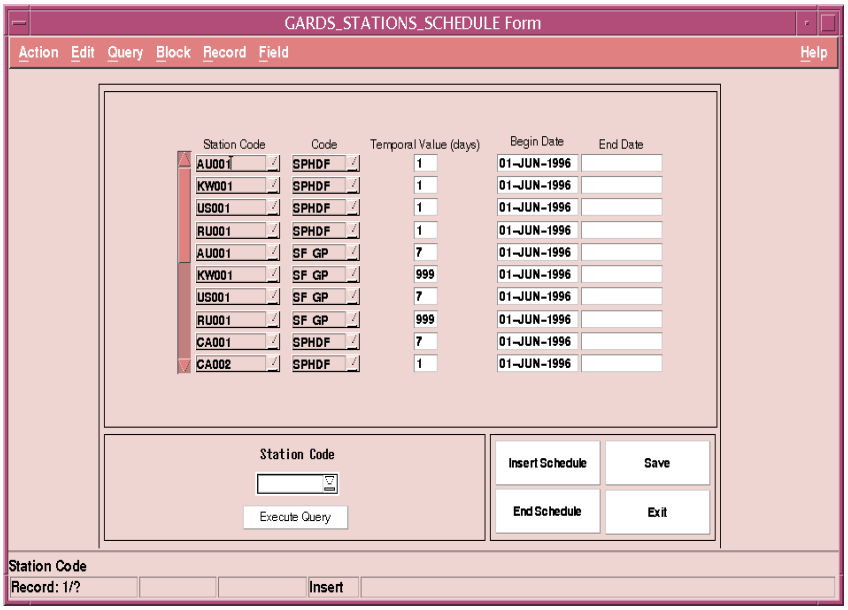

FIGURE 73. STATIONS SCHEDULE FORM

Adding a Station Schedule

To add a station to the RMS database, proceed as follows.

1. From the RMS DWB List of Forms, click STATIONS SCHEDULE.

   The Stations Schedule Form appears.

2. Click Insert Schedule.

   A blank row is inserted into the form with pull-down menus attached to the appropriate columns. The current date is automatically entered into the Begin Date column.

3. Select entries for each of the pull-down menus provided.

   Data is automatically inserted into the Station Code and Code columns.

4. Select the Temporal Value (days)box in the next column, and enter a numeric value for the new entry.

5. Click Save.

   Repeat these steps to add additional stations.

6. Click Exit.

   You are returned to the RMS DWB List of Forms.

Archiving a Station Schedule

To archive a station, proceed as follows.

1. From the Stations Schedule Form, select the Station Code to be archived and click End Schedule.

   The current date is automatically inserted into the End Date column.

2. Click Save.
3. Repeat these steps to archive additional station schedules.
4. Click Exit.

   You are returned to the RMS DWB List of Forms.

Executing a Query

To query the RMS database, proceed as follows.

1. At the bottom of the Stations Schedule Form, select an entry from the Station Code pull down menu and click Execute Query.

   All entries associated with the chosen station code will be displayed. By clicking the Execute Query button a second time, all entries in the form will be redisplayed.

2. Click Exit.

   You are returned to the RMS DWB List of Forms window.

Update Parameters Form

The Update Parameters Form, Figure 74, provides the ability to insert, modify or delete the update specific parameters utilized in the energy and resolution update routines by the Canberra processing software. This form is associated with the **gards_update_params_template** table in [IDC5.1.1Rev3].

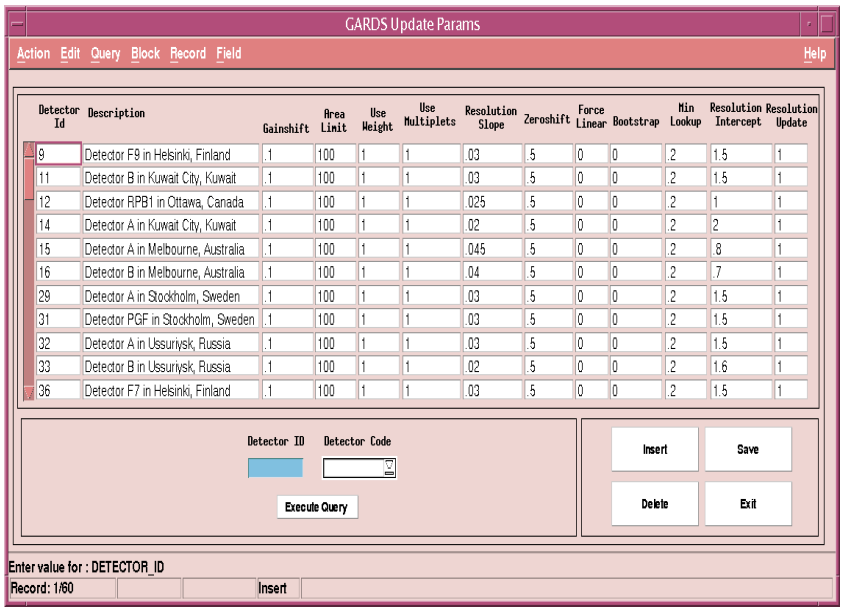

FIGURE 74. UPDATE PARAMETERS FORM

Note: spectra from each detector are analyzed according to that detector's processing parameters.

Inserting/Modifying Parameters

To insert new detector update parameters, proceed as follows.

1. From the RMS DWB List of Forms, click PROCESS PARAMS.

   The Processing Parameters Form appears.

2. Click the INSERT button.
3. The prompt, "`You must enter a detector and station ID for the new record. Do you wish to copy default data to the remaining entries?`" appears. Choosing Yes copies the current default parameters into the new record.
4. Assign the correct Detector ID to the new record.
5. Press the Tab key or select a field to change update parameters as necessary.
6. Click Save.
7. Repeat steps 2 through 6 to insert new detector update parameters.
8. Click Exit.

   You are returned to the RMS DWB List of Forms.

Modifying Parameters

This form may also be used to modify update parameters for an existing detector. Although it is possible to manually change individual parameters as described below, it is strongly recommended that modifications be made by inserting a new record so that changes can be tracked.

To modify detector update parameters, proceed as follows.

1. From the Update Parameters Form, select the text box requiring modification and enter your change.
2. Click Save.
3. Repeat these steps to modify additional detector update parameters.
4. Click Exit.

   You are returned to the RMS DWB List of Forms.

Deleting Parameters

To delete a detector entry, proceed as follows.

1. From the Update Parameters Form, select the appropriate detector and click Delete.
2. Click Save.

   Repeat these steps to delete additional detectors.
3. Click Exit.

   You are returned to the RMS DWB List of Forms.

Executing a Query

To query the RMS database for detector update parameters, proceed as follows:

1. From the Update Parameters Form, select an entry from the Detector Code text box and click Execute Query.

   All entries associated with the chosen detector code will be displayed. By removing the Detector ID associated with the chosen detector code and clicking the Execute Query button a second time, all entries in the form will be redisplayed.
2. Click Exit.

   You are returned to the RMS DWB List of Forms window.

QC Params Form

The QC Parameters Form, Figure 75, provides the ability to insert and modify parameters used in the automated quality control tests. The parameters can be configured for each detector that provides QC spectra. This form is associated with the **gards_qcparams** table in [IDC5.1.1Rev3].

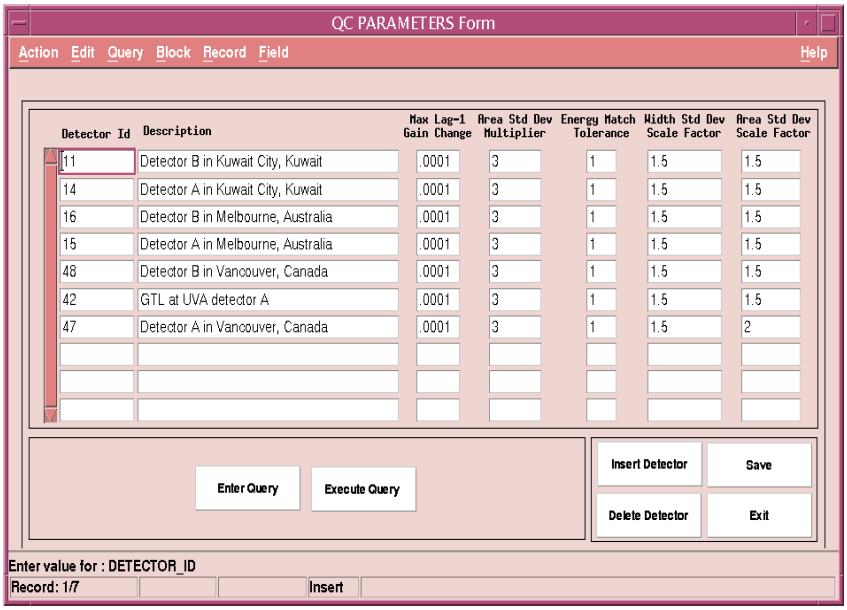

FIGURE 75. QC PARAMETERS FORM

Inserting QC Parameters

To insert a new QC parameter for a detector, proceed as follows.

1. From the RMS DWB List of Forms, click QC PARAMS.

   The QC Parameters Form appears.
2. Click Insert Detector and assign a Detector ID to the new record.
3. Press the Tab key to move among the remaining fields and enter the appropriate values.
4. Click Save.
5. Repeat steps 2 through 4 to insert additional detector specific QC parameters.
6. Click Exit.

   You are returned to the RMS DWB List of Forms.

Modifying QC Parameters

To modify a QC parameter, proceed as follows.

1. From the QC Parameters Form, select the Detector ID to be modified.
2. Select the field you want to edit and enter your changes.
3. Click Save.
4. Repeat these steps to make additional modifications to other QC parameter records.
5. Click Exit.

   You are returned to the RMS DWB List of Forms.

Deleting QC Parameters

To delete a QC parameter, proceed as follows.

1. From the QC Parameters Form, select the Detector ID to be deleted and click Delete Detector.
2. Click Save.
3. Repeat these steps to delete additional QC parameter records.
4. Click Exit.

   You are returned to the RMS DWB List of Forms.

Executing a Query

To query the RMS database for QC parameter records, proceed as follows.

1. Click Enter Query.

   The form goes blank and the Detector ID field is highlighted. Enter appropriate data.
2. Enter the detector ID for the detector to be queried.

3. Click Execute Query.

   All entries associated with the chosen detector will be displayed. By removing the Detector ID and clicking the Execute Query button a second time, all entries in the form will be redisplayed.

4. Click Exit.

   You are returned to the RMS DWB List of Forms window.

QCTargets Form

The QCTargets Form, Figure 76, allows the analyst to modify peak widths and areas for reference peaks in QC spectra. This data is used for automated QC tests. This form includes Station ID and Detector ID; station and detector descriptions; specific nuclide names and the width (channels) and area (counts) of targets; and date and time of area correction. This form is associated with the **gards_qctargets** table in [IDC5.1.1Rev3].

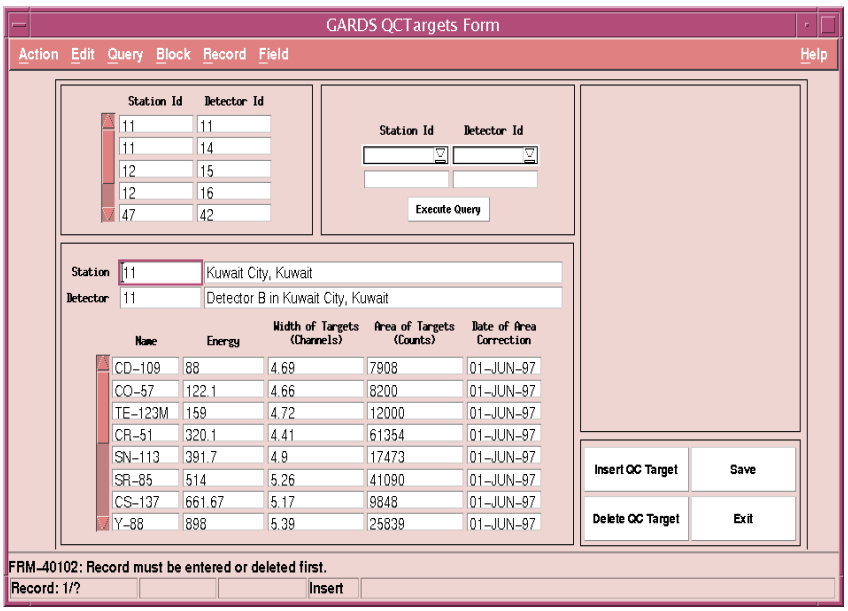

FIGURE 76. QCTARGETS FORM

Inserting QC Target Parameters

To insert a new QC target parameter, proceed as follows.

1. From the RMS DWB List of Forms, click QCTARGETS.

   The QCTargets Form appears.

2. Click Insert QC Target and assign a Station ID and Detector ID to the new record.

   If the specified Station ID and Detector ID values match existing entries in the database, the description field is automatically filled.

3. Press the Tab key to move among the remaining fields and enter the appropriate values.

4. Click Save.

5. Repeat steps 2 through 4 to insert additional detector specific QC Target parameters.

6. Click Exit.

   You are returned to the RMS DWB List of Forms.

Modifying QC Target Parameters

To modify a QC Target parameter, proceed as follows.

1. From the QCTargets Form, select the Station ID and Detector ID entry to be modified.

2. Select the field you want to edit and make the appropriate modifications

3. Click Save.

4. Repeat these steps to make additional modifications to other Station ID and Detector ID entries.

5. Click Exit.

   You are returned to the RMS DWB List of Forms.

Deleting QC Target Parameters

To delete a QC Target parameter, proceed as follows.

1. From the QCTargets Form, select the Station ID and Detector ID entry to be deleted.
2. Click Delete QC Target.
3. Click Save.
4. Repeat these steps to delete additional Station ID and Detector ID entries.
5. Click Exit.

   You are returned to the RMS DWB List of Forms.

Executing a Query

To query the RMS database for QC Target data, proceed as follows.

1. From the QCTargets Form, select one of the two text boxes in the Execute Query section.

   A pull-down menu appears.
2. Select an entry and click Execute Query.

   All entries matching your query will automatically appear.
3. To execute another query, repeat these steps.
4. Click Exit.

   You are returned to the RMS DWB List of Forms.

Reflines Form

The Update Reflines Form, Figure 77, allows the user to insert or modify refline lists used in the energy update routine of the Canberra processing software. The update refline lists are specific to Station ID, Detector ID, Data Type, and Spectral Qualifier parameters. This form is associated with the **gards_update_reflines** table in [IDC5.1.1Rev3].

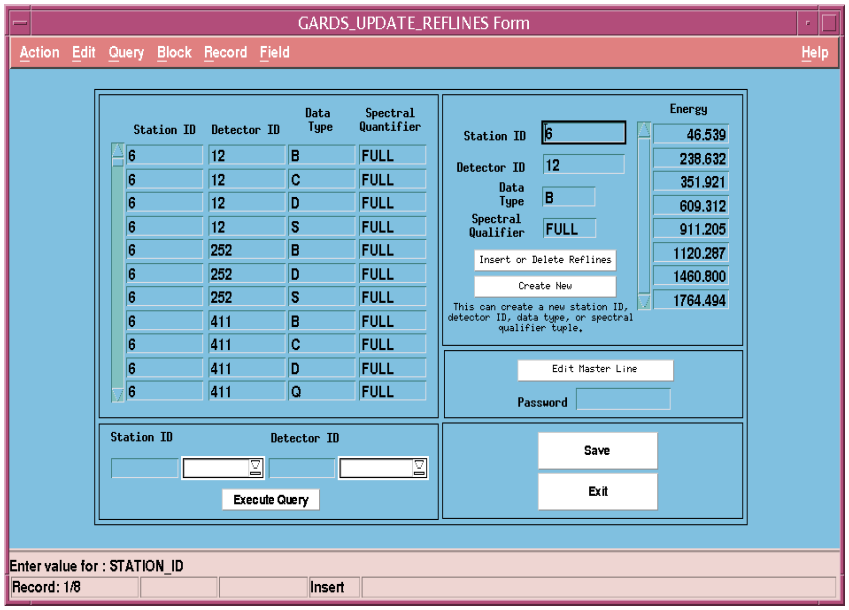

FIGURE 77. UPDATE REFLINES FORM

Additional forms are displayed when certain buttons (Insert or Delete Reflines, Create New, and Edit Master Line) are clicked in the Update Reflines form. Each of these additional forms will be discussed in the following sections.

Inserting New Refline Lists

To create new refline lists, proceed as follows.

1. From the RMS DWB List of Forms, click REFLINES.

   The Update Reflines Form appears.

2. Using the pull-down menus provided next to the Station ID and Detector ID fields in the Query section, choose the appropriate Station Code and Detector Codes and click Execute Query.

   Any entries already assigned to that station/detector combination are displayed. Note that there may be no entries currently assigned.

3. Click Create New.

   A Create Default Refline form appears. The Station ID and Detector ID values previously chosen are displayed.

4. From the Data Type, Spectral Qualifier, and Calibration Type pull-down menus, choose the appropriate values for the new record.

5. Choose Show Reflines.

   The reflines present in the Master Reflines list for the designated Data Type, Spectral Qualifier, and Calibration Type are displayed in the far column of the Create Default Refline form.

6. Click in the appropriate energy row to add a refline.

   The chosen energy lines will appear in the next column to the left. (If you mistakenly click the wrong refline, click the entry in the left column and it will be deleted from the list.)

   If no energy reflines are displayed, it indicates that there are no entries in the Master Reflines list based on the chosen parameters. To continue, you must insert reflines into the Master Reflines list. To add energy reflines, proceed as follows.

   – In the Update Reflines Form, enter your password in the Password text box. Click Edit Master Line.
     The Edit Master Reflines form appears. (If you do not have a password, the person(s) responsible for maintaining the Master Reflines must proceed with the remaining steps.)
   – Query the list by using the Query on Data Type pull-down menu.
   – Click Execute Query.
     A list of all refline entries for the specified Data Type are displayed.
   – To enter a new energy refline, click Insert Master Line.
     A blank row appears.
   – Enter the refline energy value. This energy should be identical to the energy of a known nuclide line that is generally observed in spectra of that Data Type from the station/detector combination selected.

- Use the pull-down menus provided in the form to fill in the remaining columns.
- Continue to insert reflines by repeating the steps above. When complete, click Save Changes.
- Click Return to Main Form. The Edit Master Reflines form disappears and the you are returned to the Update Reflines Form.

7. When all energy reflines are correct, click Save Changes.
8. The prompt, "`Commit changes to form?`" appears. Choose OK to commit, or Cancel.
9. Click Return to Main Form.

   The Create Default Refline form disappears and you are returned to the Update Reflines Form.
10. Click Save.
11. Repeat steps 2 through 10 to insert additional refline lists for each of the Data Type values.
12. Click Exit.

    You are returned to the RMS DWB List of Forms.

Modifying Refline List Entries

To modify an existing refline list, proceed as follows.

1. From the Update Reflines Form, use the pull-down menus for the Station ID and Detector ID fields in the Query section to select Station Code and Detector Codes values
2. Click Execute Query.

   Any entries already assigned to the chosen station/detector combination are displayed.
3. Select the appropriate Data Type by clicking in the appropriate row.
4. Click Insert or Delete Reflines.

   A new form, Insert Multiple Reflines, appears.

5. If the Data Type chosen was “C” or “Q”, then the prompt, “`Press OK to enter calibration type or CANCEL to use default value.`” appears. Click OK to choose from the different Calibration Types, or Cancel to default to the MIX Calibration Type.
6. Add reflines from the list in the far right column by clicking in the appropriate energy row, or remove reflines from the current list by clicking in the energy row in the center column.
7. Click Save Changes. The prompt, “`Commit changes to form?`” appears. Choose OK to commit, or Cancel.
8. Click Return to Main Form.

   The Insert Multiple Reflines form disappears and you will be returned to the Update Reflines Form.
9. Click Save.
10. Repeat these steps to insert additional refline lists for each of the Data Type values.
11. Click Exit.

    You are returned to the RMS DWB List of Forms.

Xenon Library

The Xenon Nuclide Libraries Form, Figure 78, allows the analyst to modify gamma lines; write database library information to a special nuclide library file (`xxxx.nlb`); and insert, modify, or delete a particular nuclide from the xenon database library The nuclide library file is required by the Canberra software routines. This form is associated with the **gards_xe_nucl_lib** and **gards_xe_nucl_lines_lib** tables in [IDC5.1.1Rev3].

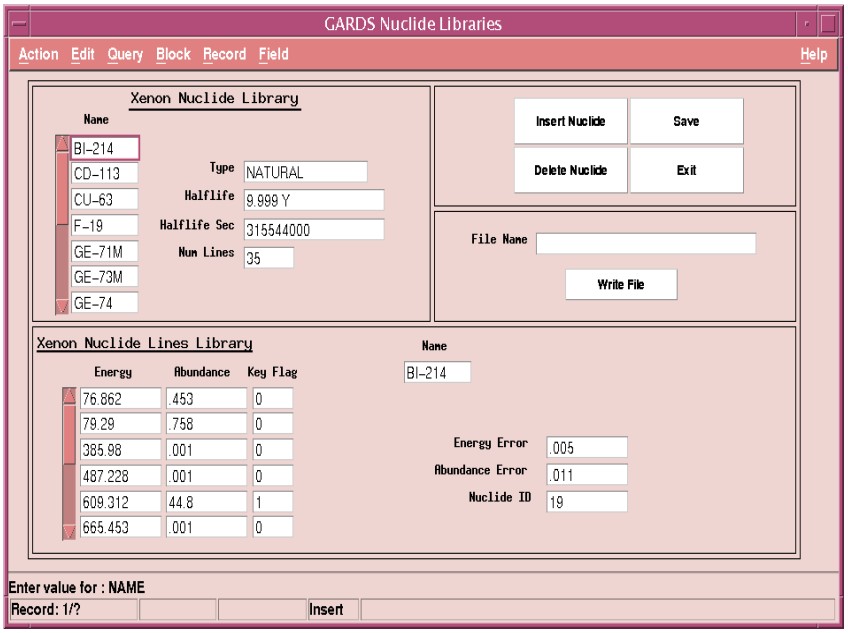

FIGURE 78. XENON NUCLIDE LIBRARIES FORM

Adding a Nuclide

To add a nuclide to the Nuclide Library, proceed as follows:

1. From the RMS DWB List of Forms, click XENON LIBRARY.

   The GARDS Nuclide Libraries Form appears.

2. Click Insert Nuclide.

   A new row appears in the Name field. Enter the nuclide to be added to the RMS database.

3. Press the Tab key to move to other data fields and enter the new Type, Halflife, and Halflife Sec into the appropriate text boxes. The Num Lines entry is based on the number of lines associated with the given nuclide as defined in the Nuclide Lines Library section of the form

4. Click Save.

5. Repeat these steps to add additional nuclides to the nuclide library.

   After the nuclide library is properly configured, write the information to an external nuclide library file by keying in a file name (`xxxx.nlb`). The automated processing uses unique `.nlb` files for each station/detector combination. The location of the file is specified in the Processing Parameters Form in the field “NID library file name.”

6. Click Exit.

   You are returned to the RMS DWB List of Forms window.

Modifying a Nuclide

To modify a nuclide in the RMS database, proceed as follows:

1. In the name field of the GARDS Nuclide Libraries Form, select the nuclide to be modified. Press the Tab key to move to the data field(s) requiring modification. and make changes
2. Click Save.

   After the nuclide library is properly configured, write the information to an external nuclide library file by keying in a file name (`xxxx.nlb`). The automated processing uses unique `.nlb` files for each station/detector combination. The location of the file is specified in the Processing Parameters form in the field “NID library file name.”

3. Select the File Name text box and enter a new file name.
4. Click Write File.
5. Click Exit.

   You are returned to the RMS DWB List of Forms window.

Deleting a Nuclide

To delete a nuclide from the RMS database, proceed as follows.

1. In the Nuclide Name field of the GARDS Nuclide Libraries Form, select the nuclide to be deleted.

2. Click Delete Nuclide.
3. Click Save.
4. Repeat these steps to delete additional nuclide records in the xenon library.
5. Click Exit.

   You are returned to the RMS DWB List of Forms.

Xenon Nuclide Lines Library

The Nuclide Lines Library section of the form displays the energy and abundance of all lines associated with a given nuclide in the Energy and Abundance columns. The Key Flag column contains either a “0” or “1,” where “1” indicates the keyline of a nuclide. Other text boxes (Energy Error, Abundance Error, and Nuclide ID) contain information associated with the nuclide-specific data.

Adding a Nuclide Line

To add a nuclide line to the Xenon Nuclide Library, proceed as follows.

1. In the Nuclide Library section of the GARDS Nuclide Libraries Form, select the nuclide requiring additional lines.
2. From the Nuclide Lines Library section, select an Energy box.
3. Click Insert Line.

   A blank row appears below the selected nuclide line. Enter information into each text box.
4. Click Save.

   The line is added to this nuclide in the Nuclide Library.
5. Repeat these steps to add additional lines.
6. Click Exit.

   You are returned to the RMS DWB List of Forms.

Modifying a Nuclide Line

To modify a line in the Xenon Nuclide Library, proceed as follows:

1. In the Nuclide Library section of the GARDS Nuclide Libraries Form, select the nuclide to be modified.

   In the Nuclide Lines Library section, the selected nuclide appears in the Name box and its associated information is loaded into the Energy, Abundance, and Key Flag columns.
2. Select the Energy to be modified.

   This activates the other text boxes in the Nuclide Lines Library and displays related information.
3. To change any nuclide line information in the Nuclide Lines Library section, select the appropriate text box and enter the data.
4. Click Save.

   The nuclide line is modified in the nuclide library.
5. Repeat these steps to add additional lines.
6. Click Exit.

   You are returned to the RMS DWB List of Forms.

Deleting a Nuclide Line to a Nuclide

To delete a line from the Xenon Nuclide Library, proceed as follows.

1. In the Nuclide Library section of the Nuclide Libraries Form, select the nuclide whose line(s) is to be deleted.
2. From the Nuclide Lines Library, select the Energy box containing the line to be deleted.
3. Click Delete Line.

   The selected energy line is removed.
4. Click Save.

   This line is removed from this nuclide in the Nuclide Library.

5. Repeat these steps to remove additional lines.
6. Click Exit.

   You are returned to the RMS DWB List of Forms.

Writing Library Information to a File

Information in the Nuclide Library can be saved to a postscript file as follows:

1. After making changes to the Nuclide Library, enter a file name (including the specific path) in the File Name box.
2. Click Write File.

   A postscript file is created.

Chapter 9: Processing Tools Procedures

This chapter provides step-by-step instructions for using the Processing Tools Radionuclide software and includes the following sections:

- Overview
- Feature-specific Procedures

Chapter 9: Processing Tools Procedures

OVERVIEW

The function of the Processing Tools software is to provide the ability to manually initiate many key automated processes. The Processing Tools software is a group of UNIX command-based tools. No menus, functions, or processes are accessed unless manually invoked at the UNIX prompt. Below is a list of the Processing Tools discussed in this chapter.

FEATURE-SPECIFIC PROCEDURES

This section provides detailed instructions for using the Processing Tools. Each tool is a stand-alone function that is invokes individually.

Multiple Analyst Review Automatic Processing

In the pipeline, *rms_mar_auto* is executed when radionuclide samples arrive at the IDC. The script *rms_pl_check* is called with the config file “rms_mar.sql” to determine if *rms_mar* should be executed for a sample. In order for a sample to be automatically assigned using *rms_mar_auto*, it must have a spectral qualifier of FULL, a data type of S, and a status of P. If these criteria are not met in full, the sample is not assigned and can be viewed as "read only" in Inspectra. Next, *rms_mar_auto* checks whether the station from which the sample originated has been assigned to a user. If the station ID is assigned to an analyst, then the sample is assigned to that analyst and subsequently appears in the analyst’s Sample Assignment Queue. If the station is not assigned to an

analyst, the sample is assigned to a special user called "unassigned." Note that all samples not assigned to analysts will be "read only" and functionality in Inspectra will be limited.

The *rms_mar_auto* process can be run from the command line as follows:

```
rms_mar_auto [-h] <-l login | -dl> -s sample_id
```

`-h`	help
`-l`	login (password entered at prompt)
`-dl`	default login read from param file $RMS_PAR
`-s`	sample ID receiving database update

Note: REQUIRED arguments include: `-s` <sample Id> and either `-l` <login name> or `-dl`.

Manual RMS Analyze Processing

The purpose of the *rms_analyze* process is to find Gaussian-shaped peaks in gamma spectra and associate those peaks with nuclides from the nuclide library. Results of this analysis, which include information about the identified peaks and nuclides, are stored in the RMS database. *Rms_analyze* is the first process executed from the pipeline on such data. If the sample data type is a QCPHD and errors occur during analysis, notifications will be sent to the subscribers of QC warnings and QC errors.

Using *rms_analyze*, a user can also reanalyze a sample with different parameters. This is useful if the original analysis failed or if the original analysis results were poor. To do this, proceed as follows:

WARNING: Running this analysis overwrites any previous results and comments made to the sample! Only database users with the proper permissions are capable of executing this command.

1. For a usage summary, at the prompt enter `rms_analyze -h` and press the Return key.

   A message appears with an example usage string and argument definitions below.

■

```
Usage: rms_analyze [-h] <-l login | -dl> -s sample_id
```

-h: help

-l: login (password entered at prompt)

-dl: default login read from param file $RMS_PAR

-s: sample id to be analyzed

Note: one of -l, -dl required.

Optional flags (`true`|`false` means either true or false):

```
============    _PROC_PARAMS_TEMPLATE    (CI    params)
================================
```

```
 [-b true|false type] Override do_back.  'type' only
required when override is set to true.  type = 'B'lank
or 'D'etector background.

 [-c true|false] Override crit_level. crit_level causes
peaks whose indicated area is below a fixed multiple of
the estimated baseline standard deviation to be
deleted.

[-ps value] Override peak_start.  Peak processing start
energy (keV). value = an integer

[-pe value] Override peak_end. Peak processing end
energy (keV). value = an integer

[-n value] Override NID confidence threshold,
nid_confid. value = a float of the form n.nnnnn

[-p value] Override peak detection threshold,
```

peak_sense. value = a float of the form n.nnnnn

[-fs true|false] Override fit_singlets; if false, singlet areas are calculated using a simple channel summation.

[-ff true|false] Override fix_fwhm; if true, widths are notestimated but are taken from RER.

[-mw value] Override default ROI width for MDC calculations. value = a float of the form n.nn

============_UPDATE_PARAMS_TEMPLATE (non-CI params) ==========
===

[-a value] Override area_lim param. This is the minimum useable peak area for inclusion in matching. value = a float of the form nnnn.n

[-dr true|false] Override do_reru param. Normally, the resolution update is performed. If overriden, the initially chosen rer coefficients will be used throughout the analysis process.

============OTHERS ==================================

[-at value] Area threshold for skinny peak rejection. value = a float of the form nnnnn.n

[-wt value] Width threshold for skinny peak rejection. value = a float of the form n.nnn

[-e b0,b1,b2,b3] Manual ECR entry for first peak search. This, and -r below, are used when the MRP ECR and/or RER are not good representations of the current system state, and external estimates are available. Be

sure to include 0's for terms not in equation. Note: you must also use the -t option when using this option.
b0 = a float of the form n.nnnnnn or n.nnnne+/-x

b1 = a float of the form n.nnnnnn or n.nnnne+/-x

b2 = a float of the form n.nnnnnn or n.nnnne+/-x

b3 = a float of the form n.nnnnnn or n.nnnne+/-x

[-initialecr value] Starting ECR for Update calculation. Value is one of the following:

C Use manual ECR as starting point for update.

M Use MRP ECR as starting point for update.

Q Use MRPQC ECR as starting point for update.

I Use Import ECR as starting point for update.

[-finalecr value] ECR analysis should use regardless of scoring. Value is one of the following:

C Use manual ECR as starting point for update.

M Use MRP ECR as starting point for update.

Q Use MRPQC ECR as starting point for update.

I Use Import ECR as starting point for update.

[-r b0,b1] Manual RER entry for first peak search.
b0 = a float of the form n.nnnnnn or n.nnnne+/-x

b1 = a float of the form n.nnnnnn or n.nnnne+/-x

[-t value] Manual input library lookup tolerance. If present, this will be used in place of the calculated value. (Must be present when using -e.) value = a float of the form n.nnnnn

[-d] By choosing this option, analysis will search for

```
efficiency coeffs (from the most-recent-prior (MRP)
sample of the same type.)  If no MRP sample exists, use
transmitted effic data set to calculate the efficiency
coeffs.
```

2. To submit a sample into the manual rms_analyze process, enter the desired argument(s) in any order and press the Return key.

   A prompt appears requesting your password.

3. Enter your password and press the Return key.

   The results of the analysis process will be displayed in the same terminal window in which you ran *rms_analyze*.

Manual RMS Categorize Processing

The purpose of the *rms_categorize* process is to prioritize the sample based on the nuclides identified from the *rms_analyze* process. *Rms_categorize* is called from the pipeline immediately after the *rms_analyze* process finishes. *Rms_categorize* calculates the priority level for the sample, based on the nuclides identified and their calculated concentrations, and stores the priority level in the database. These results are displayed during the interactive review process. When an analyst releases a sample, the same *rms_categorize* process routines are called and the updated results are stored as the categorization level for the sample.

1. For a usage summary, at the prompt enter `rms_categorize` and press the Return key.

   The message below appears with an example usage string and argument definitions:

   ```
   Usage: rms_categorize [-h] <-l login | -dl> -s sample_id
   -h:   help
   -l:   login (password entered at prompt)
   -dl:  default login read from param file $RMS_PAR
   -s:   sample id to be categorized
   Note: one of -l, -dl required.
   ```

2. To submit a sample into the manual *rms_categorize* process, enter the sample ID and login into the usage string and press the Return key. A prompt appears requesting your password.
3. Enter your password and press the Return key.

Manual RMS DB Flags Processing

The purpose of the *rms_DB_flags* process is to run a series of data quality tests that compare the analysis results for a given sample to a set of static test requirements. *rms_DB_flags* is called from the pipeline immediately after the *rms_categorize* process for particulate samples only.

All error messages from *rms_DB_flags* are written to a standard error. The standard error is redirected to `$RMS_LOG/DBflags` when called from *rms_process*.

The following is an example of the results from the *rms_DB_flags* process (as reported in an RRR):

```
Name                      Pass/Fail    Value         Test
FlowRate                  PASS         955.027       >500
Ba140_MDC                 PASS         6.99825       <30
Be7_FWHM                  FAIL         1.71421       <1.7
K40_LocationDifference    PASS         0.0324707     <3*std deviation
NormalizedGainDifference  FAIL         0.00033915    <0.0001
```

The first three tests are sample specific in that they compare the analysis results to static test requirements. The last two tests compare the energy calibration results of the current sample to a previous sample from the same detector.

1. For a usage summary, at the prompt enter `rms_DB_flags` and press the Return key.

   The message below appears with an example usage string and argument definitions:

   ```
   Usage: rms_DB_flags [-h] -s sample_id <-l login [-dl]
   -h:   help
   -s:   sample id to report
   -l:   login (password entered at prompt)
   -dl:  default login read from $RMS_HOME/rms.par
   Note: one of -l, -dl required.
   ```

2. To submit a sample into the manual *rms_DBflags* process, enter the sample ID and login into the usage string and press the Return key.

   A prompt appears requesting your password.

3. Enter your password and press the Return key.

Manual RMS PHD Report Processing

The purpose of the *rms_phd_report* process is to retrieve a raw PHD file and copy it to another specified file. If no filename is given, the file will be labeled `phd_<sample_id>.ascii` and will be written to the directory from which the executable was run.

1. For a usage summary, at the prompt enter `rms_phd_report` and press the Return key.

   The message below appears with an example usage string and argument definition:

   ```
   Usage: rms_phd_report [-h] <-l login | -dl> -s
   sample_id [-file filename]
     -h:   help
     -l:   login (password entered at prompt)
     -dl:  default login read from param file $RMS_HOME
     -s:   sample id to report
    Note: one of -l, -dl required.
   ```

   The last argument is used to designate a specific path/file name. The *rms_phd_report* process directs the output to that path/file name.

2. To submit a sample into the manual *rms_phd_report* process, enter the sample ID and login into the usage string and press the Return key.

   A prompt appears requesting your password.

3. Enter your password and press the Return key.

Manual RMS RRR Report Processing

The purpose of the *rms_rrr_report* process is to produce a Reviewed Radionuclide Report for a specific sample. The report includes sample information, MDCs, an activity summary, peak search results, SROI editing, peak search notes, processing parameters, update parameters, data quality flags, event screening flags, calibration equations, and field of regard information.

1. For a usage summary, at the prompt enter `rms_rrr_report`, without any arguments, and press the Return key.

   The message below appears with an example usage string and argument definitions:

   ```
   Usage: rms_rrr_report [-h] -s sample_id [-f filename]
   [-l login] [-dl]
   -h:   help
   -s:   sample id to report
   -f:   generate an ascii report with specified name
   -l:   login (password entered at prompt)
   -dl:   default login read from $RMS_HOME/rms.par
   Note: one of -l, -dl required
   ```

2. To submit a sample into the manual *rms_rrr_report* process, enter the sample ID and login into the usage string and press the Return key.

   A prompt appears requesting your password.

3. Enter your password and press the Return key.

Manual RMS SSREB Report Processing

The purpose of the *rms_ssreb_report* process is to create a Standard Screened Radionuclide Event Bulletin for a sample or Fission Product ID (FPID). The SSREB report includes event information; event location; station, sample, and categorization data; and laboratory results.

1. For a usage summary, at the prompt enter `rms_ssreb_report` and press the Return key.

   The message below appears with an example usage string and argument definitions.

```
Usage: rms_ssreb_report [-h] [-s sample_id] [-fpid]
fpid] [-ascii] [-html] [-asciiFile filename] [-htmlFile
filename] [-revid id] [-l login] [-dl]
-h:   help
-s:   sample id to report
-fpid:   fpid to report
-ascii:   generate an ascii report
-html:   generate an html report
-asciiFile:   generate an ascii report with specified
name
-htmlFile:   generate an html report with specified
name
-revid:   generate report using revision id
-l:   login (password entered at prompt)
-dl:   default login read from $RMS_HOME/rms.par
Note: one of -l -dl required.
one of -ascii, -html, -asciiFile, -htmlFile required
one of -s, -fpid required
```

   To process a sample through the manual *rms_ssreb_report* process, a sample must have been characterized as an event. If the sample does not contain a fission product, a message responds, "`Select an fpid or valid sample id.`" In most cases, when manually processing an SSREB report, the FPID is used rather than the sample ID.

2. To submit a sample into the manual *rms_ssreb_report* report, enter the desired argument(s) into the usage string and press the Return key. A prompt appears requesting your password.

3. Enter your password and press the Return key.

   This process creates a new file with the SSREB followed by the FPID and output type (for example, ASCII or html).

Manual RMS RNPS Report Processing

The purpose of the *rms_rnps_report* process is to generate a Radionuclide Network Product Summary (RNPS) report. The RNPS shows the radionuclide products received or generated at the IDC between two designated dates.

1. For a usage summary, at the prompt enter `rms_rnps_report`, without any arguments, and press the Return key.

   The message below appears with an example usage string and argument definitions:

   ```
   Usage: rms_rnps_report [-h] [-start startdate] [-stop
   stopdate] [-f filename] [-l login] [-dl]
   -h: help
   -start:  start date of report data in the format YYYY/
   MM/DD
   -stop: stop date of report data in the format YYYY/MM/
   DD
   -f: name of file to be generated
   -l: login (password entered at prompt)
   -dl: default login read from $RMS_HOME/rms.par
   Note: one of -l -dl required. You must have either both
   -start and -stop or neither of them. If neither -start
   nor -stop is passed in then the default (four days
   prior for three consecutive days) is used.
   ```

2. To submit a sample into the manual *rms_rnps_report* process, enter the desired argument(s) into the usage string and press the Return key.

   A prompt appears requesting your password.

3. Enter your password and press the Return key.

Manual RMS Pairs Processing

The purpose of the *rms_pairs* process is to generate a flat file that contains the calibration pair datasets utilized in the analysis of a specified sample. If no file name is given, the file is named `<station_code>-<sample_id>.pairs`.

1. For a usage summary, at the prompt enter *rms_pairs* and press the Return key.

   The message below appears with an example usage string and argument definitions.

   ```
   Usage: rms_pairs [-h] <-l login -dl> -s sid [-f file]
   -h: help
   -l: login (password entered at prompt)
   -dl: default login read from param file $RMS_PAR
   -s: sample id to open
   -f:    output    file,    default    <station_code>-
   <sample_id>.pairs
   Note: one of -1, -dl required.
   ```

2. To submit a sample into the manual *rms_pairs* process, enter the desired arguments into the usage string and press the Return key

   A prompt appears requesting your password.

3. Enter your password and press the Return key.

   The first two columns contain the peak energy and corresponding channel data from the ECR calibration dataset. The next two columns contain the peak energy and corresponding resolution data from the RER calibration dataset. The next three columns contain the peak energy and corresponding efficiency and efficiency uncertainty from the EER calibration dataset. The first row of the last column contains the highest channel number associated with the sample, while the remaining rows of the last column provide the sample ID number.

Manual RMS DB to CNF Processing

The purpose of the *rms_db_to_cnf* process is to create a Canberra-specific binary configuration file (`.cnf`) for a sample in the RMS ORACLE database. The file generated is used in the Canberra analysis software routines.

1. For a usage summary, at the prompt enter `rms_db_to_cnf` and press the Return key.

   The message below appears with an example usage string and argument definitions.

   ```
   Usage: rms_db_to_cnf [-h] -s sample_id -f file [-l
   login] [-dl]
   -h:   help
   -s:   sample id of certificate
   -f:   filename for .cnf output file
   -l:   login (password entered at prompt)
   -dl:  default login read from $HOME/rms.par
   Note: one of -l, -dl required.
   ```

2. To create a `.cnf` file, enter the desired arguments into the usage string and press the Return key.

   A prompt appears requesting your password.

3. Enter your password and press the Return key.

Manual RMS DB to NLB Processing

The purpose of the *rms_db_to_nlb* process is to create a Canberra-specific binary nuclide library (`.nlb`) file from the nuclide library in the RMS ORACLE database. The nuclide library used by *rms_analyze* in the automated analysis process must be in the Canberra-specific `.nlb` file format. This is specified in **gards_proc_params.***nuclide_lib* in [IDC5.1.1Rev3].

To create an RMS nuclide library file using the manual *rms_db_to_nlb* process, proceed as follows.

1. For a usage summary, at the prompt enter `rms_db_to_nlb` and press the Return key.

   The message below appears with an example usage string and argument definitions:

   ```
   Usage: rms_db_to_nlb [-h] <-l login | -dl> -f file -t
   <g | p>
   -h:   help
   -l:   login (password entered at prompt)
   -dl:  default login read from param file $RMS_PAR
   -f:   filename for .nlb output file
   -t:   library type - <g>as or <p>articulate
   Note: one of -l, -dl required.
   ```

2. To create an RMS nuclide library file, enter login, filename, and library type into the usage string and press the Return key.

   A prompt appears requesting your password.

3. Enter your password and press the Return key.

Manual RMS NLB to DB Processing

The purpose of the *rms_nlb_to_db* process is to load data into the RMS ORACLE database from a Canberra-specific binary `.nlb` file. The nuclide library used by *rms_analyze* in the automated analysis process must be in the Canberra-specific `.nlb` format. This is specified in the *nuclide_lib* field of the **gards_proc_params** table in [IDC5.1.1Rev3]. This field specifies where a particular `.nlb` file is located. If the `.nlb` file contains the library to be used with other radionuclide software applications, the appropriate library must be loaded into the RMS ORACLE library tables. Inspectra displays the data contained in the RMS ORACLE library tables.

1. For a usage summary, at the prompt enter `rms_nlb_to_db` and press the Return key.

   The following usage string and argument definitions appear.

   ```
   Usage: rms_nlb_to_db [-h] <-l login | -dl> -f file -t
   <g | p>
   -h:   help
   -l:   login (password entered at prompt)
   -dl:   default login read from param file $RMS_PAR
   -f:   filename for .nlb input file
   -t:   library type - <g>as or <p>articulate
   Note: one of -l, -dl required.
   ```

2. To load an RMS nuclide library file into the RMS database, enter login, filename, and library type into the usage string and press the Return key.

   A prompt appears requesting your password.

3. Enter your password and press the Return key.

Manual RMS Analyze Categorize DBFlags (ACD) Processing

The purpose of the *rms_acd* process is to run the following executables consecutively: *rms_analyze*, *rms_categorize*, and *rms_DB_flags*. *rms_acd* does not work with Beta-Gamma sample. Since *rms_acd* uses the automatic login (-dl), it should never be used after an analyst has made updates to the sample. If a sample has been updated in the manual database, the these executables must be run in the manual database.

1. There is no usage summary available. At the prompt, enter *rms_acd* and press the Return key.

   The following prompt appears: "`Enter Sample id:`"

2. Enter the Sample ID and press the Return key.

   The following prompt appears: "`Are you sure you want to process sample <sample_id> (y/n)`."

3. Enter "`y`" to start the *rms_acd* process or "`n`" to cancel, and press the Return key.

Manual RMS Xenon Analyze Processing

The purpose of the *rms_xanalyze* process is to execute the xenon beta-gamma coincidence data analysis routine. Results of this analysis are stored in the RMS database. *Rms_xanalyze* is the first process executed from the pipeline on 3-D beta-gamma coincidence PHD files.

WARNING: Running this analysis overwrites any previous results and comments made to the sample! Only database users with the proper permissions are capable of executing this command.

1. For a usage summary, enter `rms_xanalyze` and press the Return key.

   The message below appears with an example usage string and argument definitions.

   ```
   rms_xanalyze [-h] <-l login | dl> -s sample_id
   -h:   help
   -l:   login (password entered at prompt)
   -dl:  default login read from param file $RMS_PAR
   -s:   sample id to analyze
   Note: one of -l, -dl required.
   ```

2. To submit a sample into the manual *rms_xanalyze* process, enter the sample ID and login into the usage string and press the Return key.

   A prompt appears requesting your password.

3. Enter your password and press the Return key.

   The results of the analysis process will be displayed in the same terminal window in which you ran *rms_xanalyze*.

Manual RMS Xenon RRR Report Processing

The purpose of the *rms_xe_rrr_report* process is to produce a noble gas version of the RRR for a specific sample. The report includes sample information, comments, MDCs, an activity summary, ROI results, ROI boundaries, event screening flags, and calibration equations.

1. To submit a sample into the manual *rms_xe_rrr_report* process, type `rms_xe_rrr_report` followed by the desired arguments (`-s <sample_id> -l <login>`) and press the Return key.

   A prompt appears requesting your password.

2. Enter your password and press the Return key.

Chapter 10: Workflow Procedures

This chapter provides step-by-step instructions for using the Workflow Radionuclide software and includes the following sections:

- Overview
- Feature-specific Procedures
- Interactive Procedures

Chapter 10: Workflow Procedures

OVERVIEW

The purpose of the radionuclide interactive processing system is to provide organized, relevant data in a format that can be used by analysts, scientists, processing engineers, and technical management for radionuclide monitoring. The RMS Workflow software is a GUI that displays receipt of data and the state of blowers and detectors at stations and laboratories with respect to time.

FEATURE-SPECIFIC PROCEDURES

This section provides detailed instructions for using the software. These procedures also identify and describe the RMS Workflow main application window, menu selections, and special dialogs.

Understanding Workflow Window Elements

The RMS Workflow application window (Figure 79) contains a data panel containing lines identifying the station blower(s) and detector(s), a graphical display of blower and detector data, numerous scroll bars, a chronological header, and a message panel. Each element is discussed in turn.

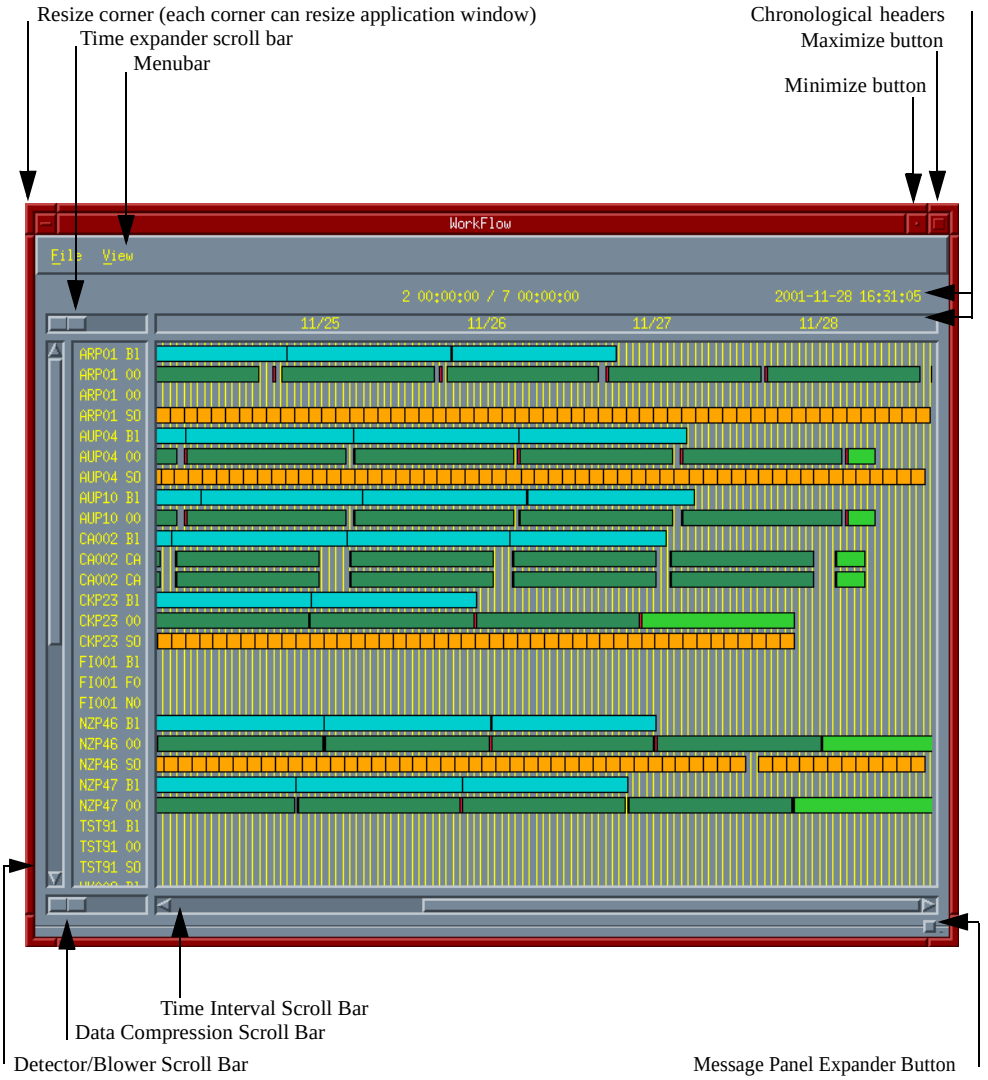

FIGURE 79. WORKFLOW APPLICATION WINDOW

Data Panel

In the Data Panel, a multi-colored bar graph displays the state of the blower and detector for a specific station over time. For each station, a line labeled “blower” indicates the times that the blower was on or off; a light blue line indicates that the blower was running and the absence of a line means that the blower was off. There is also a line for each station detector in various colors relating to the type of count that the detector completed during a given time. For an explanation of the color codes see “Menubar Selections” on page 251.

Scroll Bars

Four types of scroll bars are available:

- Time expander scroll bar

  This scroll bar expands or contracts the amount of time that can be displayed in the data panel and correlates to the first value displayed in the chronological header.

- Data compression scroll bar

  This scroll bar compresses the bar graphs so that more data can be viewed at a time and correlates to the second value displayed in the chronological header.

- Time interval scroll bar

  This scroll bar enables you to view entire bar graphs, as specified by the time expander and data compression scroll bars.

- Detector/blower scroll bar

  This scroll bar enables you to view all of the station detectors and blowers currently in operation.

Chronological Headers

The first header shows incremental time periods and the number of days that can be viewed in the display panel. Both time periods are defined by the Time Expander and the Data Compression scroll bars. The second header shows that the bar chart is based on 4-hour incremental time periods (UTC).

Message Panel

The RMS Workflow message panel provides software operating messages and is rarely used for viewing radionuclide data. To expand this panel, select the Panel Expander button. The arrow will turn into a cross-hair. Drag the button upward. The Data Panel becomes smaller and messages can be viewed in this panel. To view all messages contained in the Message Panel, use the Message Panel Scroll Bar to move through data that may not be immediately visible.

Menubar Selections

The RMS Workflow menubar contains two menus. Each menu and menu selection is described in Table 21. Following this table is a discussion of the States menu selection, other selections are self-explanatory based on the defined functions in Table 21.

TABLE 21: RMS WORKFLOW MENUS AND MENU SELECTIONS

Menu	Selection	Functions
File	Create Interval	Inactive for radionuclide data.
	Remove Block of Arrivals	Inactive for radionuclide data.
	Process Block of Intervals	Inactive for radionuclide data.
	Exit	Closes application and returns you to the UNIX prompt.
View	Update	Refreshes data displayed in the data panel.
	Reset	Resets data in the data panel based on the latest information in the RMS database.
	Clear	Clears message panel.
	Exception Intervals	Inactive for radionuclide data.
	States	Provides legend for station detector and blower states displayed in each bar graph of the data panel.

Identifying Data States

The States menu selection provides a dialog box containing both a color-code and alpha-character abbreviations to identify specific data states.

To view color coding for detector and blower states, proceed as follows:

1. Choose View --> States.

   The States dialog appears.

Table 22 provides definitions for the color-codes and abbreviations displayed in this dialog.

TABLE 22: STATES MENU SELECTION

Color	Abbreviation	Definition
Light green	PREL_SPHD	Preliminary sample count, 4-hours.
Dark green	FULL_SPHD	Full sample count, 23.5-hours.
Salmon	BLANKPHD	Blank count.
Magenta	CALIBPHD	Calibration count.
Pink	DETBKPHD	Detector background.
Red	QCPHD	Quality control.
Light blue	on	Blower is on.
Orange	SOH	Indicates reception of RMSSOH message

Analyzing Data

When reviewing radionuclide data using the RMS Workflow software, the pipeline operator visually inspects data for gaps. To investigate station activity, each segment of the color-coded bar graph provides you with detector or blower activity.

Obtaining Blower Data

As discussed, the light blue bar graph indicates that a blower is on and a blank line indicates that the blower is off. In addition to visual detail, you can review blower activity by displaying a pop-up dialog.

To review blower activity data, proceed as follows:

1. Place your pointer on the specific color-coded bar graph for the station blower of interest.
2. Click the right mouse button.

   A pop-up dialog box provides the station blower status for the bar graph that you selected. Figure 80 provides an example of a blower status dialog box for the USP70 station. The dialog box is displayed for a 24-hour period beginning July 19, 2000.

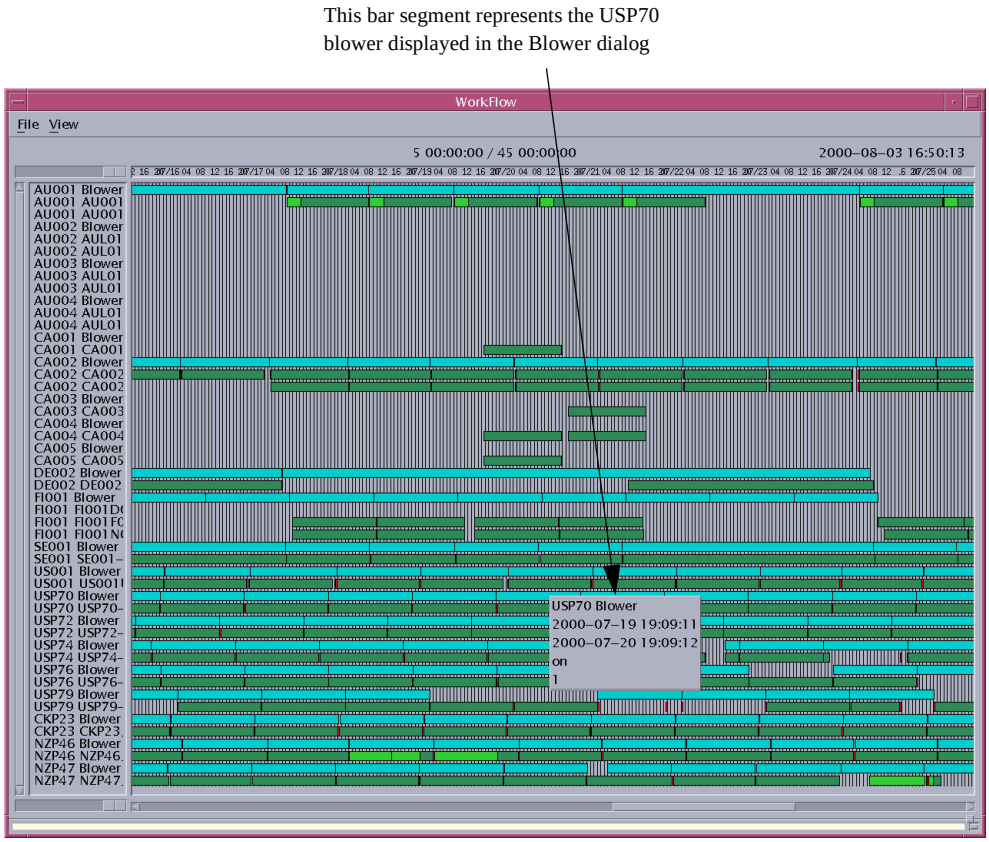

FIGURE 80. WORKFLOW POP-UP BLOWER STATUS DIALOG BOX

Information in the pop-up dialog describes the following blower information.

- Site code (USP70).
  The first two characters identify the country, the third character signifies the station type, and the last two characters are the 2-digit number assigned to the station in the CTBT text. For a list of country codes, station types and station numbers, see [IDC3.4.1Rev2].
- Blower start date and time.
  (2000-07-19 19:09:11)

- Blower stop date and time.
  (2000-07-20 19:09:12)
- Current blower status (on).
- Extra field not used for radionuclide data (1).

Obtaining Detector Data

Station detector status is displayed graphically. Each color-coded portion of the bar graph identifies data receipt, station detector status, and data types as discussed in "Identifying Data States" on page 252. In addition to a visual review, you can review detector status by displaying a pop-up dialog, as follows.

1. Position the arrow on the specific color-coded bar graph for the station detector of interest.
2. Click the right mouse button.

   A pop-up dialog box appears. Figure 81 provides an example of a station detector status box dialog for USP70.

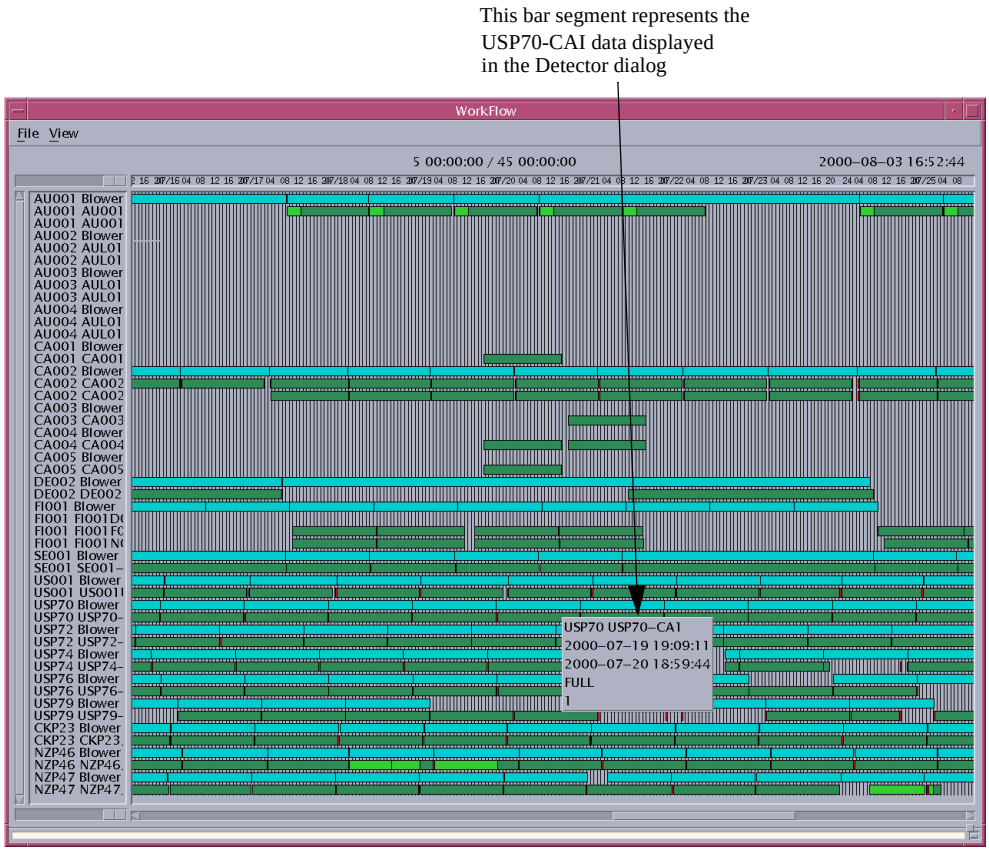

FIGURE 81. WORKFLOW STATION POP-UP DETECTOR STATUS DIALOG BOX

The following information is contained in the detector status

- Site and detector identification.
  (USP70 USP70-CAI)
- Detector acquisition start date and time.
  (2000-07-19 19:09:11)
- Detector acquisition end date and time.
  (2000-07-20 18:59:44)
- Spectral Qualifier (FULL).

– Extra field not used for radionuclide data (1).

INTERACTIVE PROCEDURES

These steps are representative of current Prototype International Data Centre procedures.

1. Visually review the data panel for receipt of information and gaps in data.
2. To determine whether the gap is expected, be familiar with a station's operating schedule.
3. If an unexpected gap is observed, you must investigate possible scenarios. Data gaps can be a result of a communication problem, station power outage, equipment problem or standard maintenance.

Chapter 11: Event Screening Procedures

This chapter describes the Data Quality and Event Screening tests and how to interpret their results. The following sections are included:

Chapter 11: Event Screening Procedures

OVERVIEW

The Data Quality and Event Screening tests provide a set of standards by which all particulate radionuclide samples are measured, either during the RMS automatic analysis process or after interactive analyst review. These tests not only provide an overview of the quality of the sample data, but also a method of interpreting the analysis results.

The radionuclide applications software incorporates a five-level characterization scheme [WGB98], as shown in Figure 82. This scheme incorporates the Categorization List for Particulate Samples (CLPS), which is a list of anthropogenic fission and activation radionuclides that are considered significant if identified by the RMS analysis process. The levels are as follows:

- Level 1 - Typical activity concentrations of radionuclides (either natural or anthropogenic) not on the CLPS are measured.
- Level 2 - Anomalous activity concentrations of radionuclides (either natural or anthropogenic) not on the CLPS are measured.
- Level 3 - Typical activity concentration of one fission product or activation product on the CLPS is measured.
- Level 4 - Anomalous activity concentration of one fission product or activation product on the CLPS is measured.
- Level 5 - Multiple anomalous activity concentrations of anthropogenic radionuclides on the CLPS are measured.

Note that some of the radionuclides contained in the CLPS are not associated with nuclear explosions.

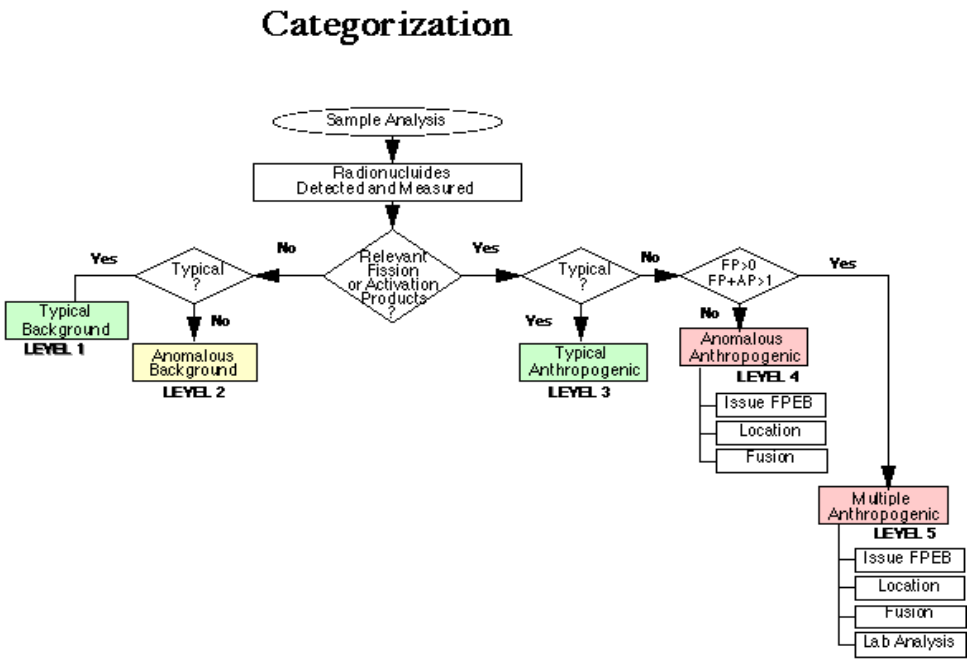

FIGURE 82. FIVE-LEVEL CATEGORIZATION SCHEME

Noble gas samples are categorized slightly different than particulate samples because of the chemical separation process the sample undergoes. This chemical separation process limits the number of radionuclides that may be present in a noble gas sample. Only xenon isotopes may be quantified with noble gas sample data. As a result, if no relevant Xe isotopes are identified in the sample, then the categorization level can only be a Level 1. It is not possible to have a Level 2 noble gas sample. This screening method is commensurate with what is suggested in [CTB99]. A diagram of the noble gas sample characterization is provided in Figure 83.

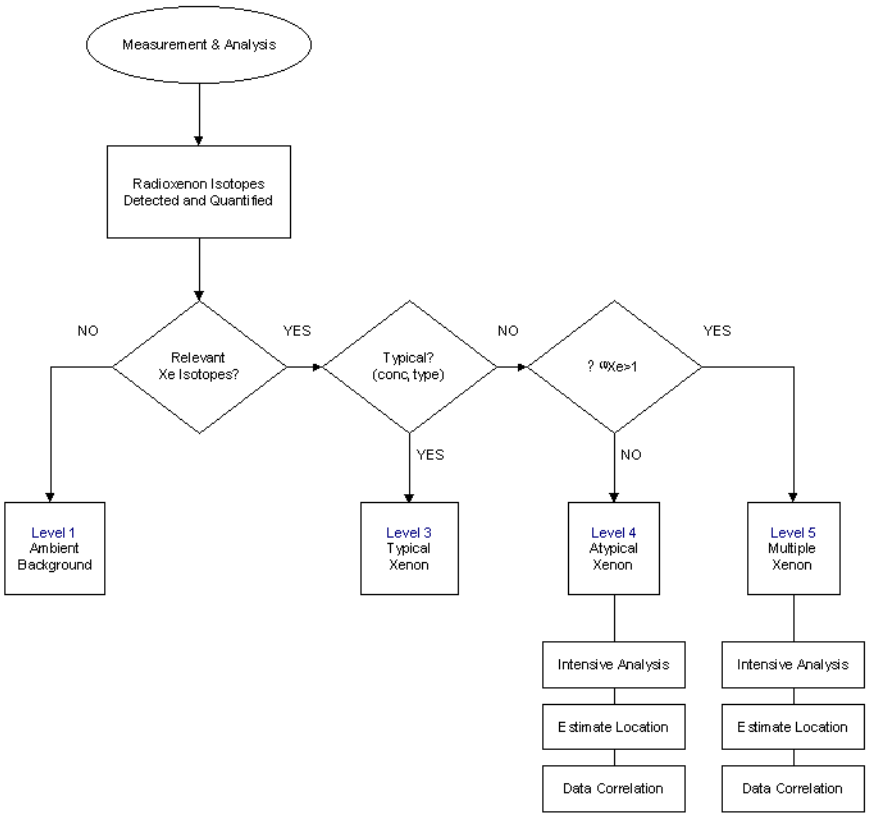

FIGURE 83. NOBLE GAS SAMPLE CHARACTERIZATION

DATA QUALITY FLAGS

A number of data quality flags are used to facilitate quality control of particulate sample data. These flags are automatically generated and stored in the RMS ORACLE Database**.** Examples of the data quality flags are provided in Table 23. The SOH data and spectral parameters used in these tests - such as FWHM and MDC calculations - provide a reliable indication of the quality of spectral data received from a given station. The results from the data quality flags are reported in the both the Automatic Radionuclide Report (ARR) and the RRR.

TABLE 23: DATA QUALITY FLAGS

Flag Name	Pass/Fail	Test
FlowRate	PASS	>500
Ba140_MDC	PASS	<30
Be7_FWHM	PASS	<1.7
K40_LocationDifference	PASS	<3*std deviation
NormalizedGainDifference	PASS	<0.0001

The Flow Rate, Ba140MDC, and Be7_FWHM tests are self-explanatory and are indicative of various aspects of station and detector performance.

The K40_LocationDifference test measures the difference in the centroid location for the ^{40}K peak in the current spectrum and the location of the ^{40}K peak in the most recent spectrum for a specific detector. An empirical formula based on the area of the peak is used to estimate the error in the ^{40}K location. The upper bound for this test is a multiple (currently 3) of the estimated standard deviation. The test is designed to detect a possible zero-shift in a detector [Eva97].

The NormalizedGainDifference test calculates a normalized gain for the current spectrum and subtracts the value of the normalized gain from the most recent spectrum for the detector. The absolute value of this difference is compared to an arbitrary constant limit (currently set to 0.0001). The test is designed to detect a possible gain shift in a given detector [Eva97].

EVENT SCREENING FLAGS

A number of event screening flags are used to provide additional information on particulate samples. These flags are generated upon the release of a particulate sample and are stored in the RMS ORACLE Database. Examples of the event screening flags are provided in Table 24. If the result of an event screening test is positive, the time since the last positive occurrence is noted. The results from the Event Screening Flags are reported in the RRR.

TABLE 24: EVENT SCREENING FLAGS

Flag Description	Results and Specifics
Activation Products present in this spectrum	Yes
Number of days since last activation product	35.888
Only one fission product in spectrum	Yes
Number of days since last fission product	1.888
2 or more fission products in spectrum	Yes
Number of days since 2 or more fission products	421.888
^{137}Cs present in spectrum	Yes
Number of times seen in last 30 days	2

The Custom Event Screening Tool is an interactive Web tool that allows you to search the IDC database using default or user-defined event screening criteria.

Once you have accessed the Web site (obtain web address, logon, and password from an authorized user of system administrator), the following options are available:

1. A map displaying the current stations,
2. Date selections that will limit the extent of the database search,
3. Categories or equations based query options, and
4. An option to define the way the query output is ordered (by station, date, or category).

Once the query is complete, the Web page updates and displays a Query Summary, indicating the options chosen and the query results. The events are numbered and the Station, Sample ID, Collect Stop, IDC Category and a link to the appropriate RRR and SSREB are provided.

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Glossary

Symbols

2-D

Two-dimensional.

3-D

Three-dimensional.

b

Beta particle.

g

Gamma ray.

μBq

MicroBecquerels.

A

abundance

Fraction of a decay event that results in the radiation(s) of interest (for example, a gamma line at a specific energy or a beta-gamma coincidence pair). Intensity is sometimes used to mean abundance.

acquisition live time

Time multichannel analyzer (MCA) electronics is available for processing pulse amplitude signals; equivalent to acquisition real-time less detector dead-time, reported in seconds.

acquisition real time

Total elapsed clock time a sample is counted, reported in seconds.

acquisition start date

Date of spectrum acquisition commencement, format is yyy/mm/dd.

acquisition start time

Time of spectrum acquisition commencement, format is hh:mm:ss.s.

acquisition stop

When the detection system at a station completes sample acquisition.

activation products

Nuclides produced from the absorption of neutrons by a nucleus.

activity

Decay rate of a radionuclide; this quantity is usually expressed in Becquerels (disintegrations per second), Bq.

ALERT

Alert message. Data type that includes ALERT_FLOW, ALERT_SYS, ALERT_TEMP, and ALERT_UPS.

amp

Amplitude.

anthropogenic

Man-made, not of natural origin.

architecture

Organizational structure of a system or component.

archive

Single file formed from multiple independent

ARR

Automatic Radionuclide Report. This report is a product of the automatic data processing and includes sections describing the sample information, prioritization results (noble gas only), sample activity, MDCs for key nuclides, peak search results and notes, processing parameters, update parameters, data quality flags, event screening flags, calibration equations, and field of regard.

ARSA

Automated Radioxenon Sampler/Analyzer.

ASCII

American Standard Code for Information Interchange. Standard, unformatted 256-character set of letters and numbers.

assay date

Date of certificate source assay, format is yyy/mm/dd.

assay time

Time of certificate source assay, format is hh:mm:ss.s.

attribute

A database column.

authentication signature

Series of bytes that are unique to a set of data and that are used to verify the authentication of the data.

AUX

Auxiliary Power Supply

AWA

Analyst Work Area; radionuclide intranet software application used to obtain a system status/state of health overview of all stations sending radionuclide information to the IDC.

B

background

Contribution to a spectrum from naturally occurring radionuclides as well as interactions between radiation and materials in the vicinity of the detector.

background measurement ID

Unique alphanumeric string identifying the relevant background measurement for a specific sample; includes the detector code and the background acquisition initiation date and time.

background subtraction

Process of removing background counts from a spectrum or a region of interest within a spectrum.

barometric pressure

Outside air pressure, expressed in hPa.

baseline

Contribution to a spectrum from the partial energy deposition of a gamma ray in a detector.

Becquerel

Unit of activity equal to one disintegration per second.

beta-gamma coincidence efficiency

Ratio of counts detected in a 2-D ROI to the actual amount of photons emitted by a sample in coincidence with an electron; depends on detector configuration, geometry, and ROI boundary limits.

beta-gamma coincidence event

Nuclear decay that produces both a gamma ray and a beta particle within a very short time scale. May also refer to other photon-electron coincidence events such as an X-ray with a conversion electron.

beta-gated gamma spectrum

Gamma spectrum in which all photons counted were detected in coincidence with an electron.

beta particle

Electron that is produced from a nuclear decay; may also refer to other electron radiations, for example, a conversion electron.

binary data files

Radionuclide analysis configuration data files in a proprietary format used by the Canberra software library.

BLANKPHD

Blank Pulse Height Data; ASCII data message transmitted to the IDC that contains the pulse height data of an unexposed air filter as well as other information in an IDC-approved format.

blank subtraction

Process of removing counts from a sample spectrum or a region of interest within a sample spectrum originating from the air filter.

Bq

Becquerel.

C

CALIBPHD

Calibration Pulse Height Data; ASCII data message transmitted to the IDC containing the pulse height data of a certified standard source as well as other information in an IDC-approved format. The data in a CALIBPHD is used to perform the ECR, EER, and RER.

calibration

Process of determining the response function and sensitivity of an instrument or its derived channel.

calibration coefficients

Numbers that define the energy, resolution, and efficiency equations.

calibration energy

Part of the energy/channel pairs that make up a detector's energy calibration data.

category

Number from 1 to 5 assigned to a radionuclide sample during interactive analysis indicating the presence of certain types of nuclides. Category 1 indicates a spectrum with normal natural nuclides while 5 indicates spectra with multiple man-made nuclides.

centroid

Energy (in keV) or channel number at the center of a fitted peak.

centroid channel

Spectrum channel at the center of a photopeak.

certificate

Certified standard source of known activity used in the acquisition of radionuclide energy, resolution, and efficiency calibration data.

certified laboratory

Radionuclide laboratories listed in Annex 1 of the CTBT, including any laboratories certified by the IMS/IDC in the future.

channel

An energy window (in keV) representing a differential increment of pulse height.

click

Select an element on the screen by positioning the pointer over the element, then pressing and immediately releasing the mouse button.

cm

Centimeter.

CMR

Center for Monitoring Research.

.cnf

Canberra Nuclear Format.

collection start date

Date of air sample collection commencement, format is yyy/mm/dd.

collection start time

Time of air sample collection commencement, format is hh:mm:ss.s.

collection stop date

Date of air sample collection termination, format is yyy/mm/dd.

collection stop time

Time of air sample collection termination, format is hh:mm:ss.s.

command

Expression that can be input to a computer system to initiate an action or affect the execution of a computer program.

comments

Free text field containing comments made by a station operator or IDC analyst.

concentration

Activity per unit volume of air.

configuration

Arrangement of computer system or component as defined by the number, nature, and interconnection of its parts.

CORIANT

Coincident Radiation Interactive Analysis Tool.

cosmic nuclides

Nuclides produced by the interaction of cosmic-rays with matter.

COTS

Commercial, Off-the Shelf.

counts

Number of pulses observed within a spectrum channel.

critical level

Minimum net counts that must be contained in an ROI for nuclide identification (L_C).

CSC

Computer Software Component.

CSCI

Computer Software Configuration Item.

CTBT

Comprehensive Nuclear Test-Ban Treaty.

D

d

Day(s).

data block

Units of information that, when combined with other data blocks, make up a data message.

data type

Kind of data in a data message; possible data types include ALERT_FLOW, ALERT_SYS, ALERT_TEMP, ALERT_UPS, ARR, BLANKPHD, CALIBPHD, DETBKPHD, GASBKPHD, MET, QCPHD, RLR, RNPS, RRR, SAMPLEPHD, and SSREB.

date of last calibration

Date of previous detector calibration, format is yyy/mm/dd.

DB

Database.

decay time

Time duration an exposed filter is allowed to decay before data acquisition.

DETBKPHD

Detector Background Pulse Height Data; ASCII data message transmitted to the IDC containing the pulse height data from a background count as well as other information in an IDC-approved format.

detector code (or ID)

Includes the radionuclide site code, plus four unique characters identifying a specific detector unit.

detector type

Data field describing the type of radiation detector used in the data acquisition process.

dialog box

Box that appears on the screen after you issue a command and requests information or a decision.

DWB

Data Work Bench; radionuclide software application that provides interaction with the RMS database.

E

ECR

Energy (vs.) Channel Regression; an equation providing the detector-specific relationship between channel number and energy. The equation contains calibration coefficients and is estimated from a transmitted calibration dataset.

ECRU

Energy (vs.) Channel Regression Update; an equation providing the detector-specific relationship between channel number and energy. The equation contains calibration coefficients and is estimated from energy-channel pairs in the current spectrum

EER

Energy (vs.) Efficiency Regression; an equation providing the detector-specific relationship between efficiency and energy. The equation contains calibration coefficients and is estimated from a transmitted calibration dataset.

efficiency

Ratio of counts detected under a photopeak to the amount of radiation quanta emitted by a sample; depends on detector configuration and geometry. This parameter is unitless.

efficiency energy

Component of the energy/channel pairs composing a detector's energy calibration data; energy at which a certain efficiency value is valid. Reported in keV.

energy

A spectral line's energy in keV.

energy span

The energy interval in which a multi-channel analyzer counts radiation quanta. Usually equivalent to the highest energy on the gamma or beta axis, rounded to the nearest 100 keV.

error in centroid channel

Difference between the spectrum photopeak centroid channel energy and the actual energy of the emitted gamma ray.

event

Occurrence that displays characteristics indicative of a possible nuclear weapons test.

EWMA

Exponentially Weighted Moving Average.

F

field of regard

An area within which air has a non-zero probability of moving over a site during a specific time interval, and is included in the ARR and RRR.

FIR

Finite Impulse Response; a digital filtering technique.

first split

First fractionation of a sample; usually performed at a sampling station to enable multiple independent analyses at different laboratories.

fission products

Nuclides produced from fission.

flow rate

Air volume passing through a blower per unit time; reported in scm (m^3)/hr.

FOR

Field of Regard.

FPID

Fission Product Identification.

FULL

Full; spectral identifier indicating that the sample has been counted for the total acquisition duration.

FWHM

Full Width at Half-Maximum; metric of detector resolution and equivalent to the width of a photopeak (in keV) taken at the peak height equal to half the maximum peak counts.

G

gain

Amplification of a photon's energy deposition signal in a detector crystal. This is achieved through the use of electronic amplifiers.

gamma

Gamma ray.

gamma-ray

Photon that is produced from a nuclear transition; may also imply other photon radiations, for example, an X-ray.

GARDS

Global Atmospheric Radionuclide Detection System; the network of radionuclide monitoring stations that meet CTBT requirements and transmit radionuclide data to the IDC with coordination by the IDC.

GASBKPHD

Gas Background Pulse Height Data. Data type sent by noble gas monitoring systems that observe a memory effect during sample acquisition due to atoms from the previous sample adsorbed onto the walls of the gas cell. The counts from the memory effect must be subtracted from the sample counts for accurate activity quantification.

GMT

Greenwich Mean Time.

GUI

Graphical User Interface.

H

h

Hour(s).

half-life

The time required for a radionuclide to decay to half its initial activity.

histogram

Two-dimensional array containing beta-gamma coincidence counts. One axis represents gamma channels (or energy) while another represents beta channels (or energy). The data in a histogram may be plotted in 3-D or as a 2-D contour plot.

HPGe

High-Purity Germanium Detector.

hr

Hour(s).

Hz

Hertz

I

ID

Identification; identifier.

IDC

International Data Centre.

IMS

International Monitoring System.

Inspectra

GUI-based tool that facilitates interactive review and analysis of the automated spectral data processing results.

intranet

Restricted-access computer network, operated and managed by an organization to share information and resources with it's members.

ISAR

International Surveillance of Atmospheric Radionuclides.

K

keV

Kiloelectron Volts; a metric of energy.

keyline

The gamma ray of a radionuclide with the highest detection probability.

L

L_c

Critical Level [Cur68].

L_D

Detection Limit [Cur68].

LEGe

Low-Energy Germanium; a type of germanium detector that is used for low-energy gamma spectroscopy.

M

m

1. Meters.
2. SI prefix meaning milli-.
3. Month(s).
4. Minute(s).

mBq

milliBequerel.

MDA

Minimum Detectable Activity

MDC

Minimum Detectable Concentration.

message ID

Unique 20-character alphanumeric identification given to a message by the sender that facilitates message tracking for the sender.

MET

Meteorological message; one of the many radionuclide data types.

MID

Measurement ID.

minimum detectable concentration

Activity concentration of a given radionuclide that is indistinguishable from the measurement process noise level.

MRP

Most Recent Prior; the sample counted most recently on the same detector and originating from the same station as the sample presently being analyzed.

multiplet

A spectrum region of interest comprised by more than one photopeak.

N

natural radioactivity

Radioactivity from cosmogenic and primordial nuclides that is always present on earth.

NDC

National Data Center.

net area

Equal to the integrated photopeak counts minus the baseline and background counts.

NID

Nuclide Identification.

NL

Nuclide Library.

noble gas

One of the noble elements in the periodic table: He, Ne, Ar, Kr, Xe, and Rn.

nuclide

One of many combinations of nucleons that may comprise an atomic nucleus. Because all nuclides of interest with respect to CTBT compliance verification are radioactive, this term is often used to refer specifically to radionuclides.

O

ODE

Ordinary Differential Equation.

online

Logged onto a network or having unspecified access to the Internet.

ORACLE

Vendor of PIDC and IDC database management system.

P

PE

Prediction Error.

peak

A statistically significant increase in counts above a spectrum baseline at an energy associated with a gamma line of a particular radionuclide or other phenomenon.

PHD

Pulse Height Data; a format for spectral data messages transmitted to the IDC. Possible PHD data message types include SAMPLEPHD, GASBKPHD, BLANKPHD, DETBKPHD, CALIBPHD, and QCPHD.

PIDC

Prototype International Data Centre.

PIF

Prediction Interval Filter.

PLSQL

Programming language for the database.

pop-up

Small window that contains selectable objects such as filter settings.

PREL

Preliminary; usually referring to a SAMPLEPHD with an acquisition time less than that of the full acquisition duration.

priority

Number from 1 to 5 assigned to a radionuclide sample during automatic analysis indicating the presence of certain types of nuclides. Category 1 indicates a spectrum with normal natural nuclides while 5 indicates spectra with multiple man made nuclides.

progeny

A radionuclide that comes into being due to the decay of a parent.

pull-down

Small list of selectable objects, such as menu items, which appears below a menu heading.

Q

QC

Quality Control.

QCPHD

Quality Control Pulse Height Data; ASCII data message transmitted to the IDC containing the pulse height data of a certified standard source as well as other information. The QCPHD, along with other information, is used to check a detector's state of health.

quantity

Collected air volume in scm; same as sampled air volume.

R

radioactivity

See activity.

radionuclide

A nuclide that has an unstable nucleus, that is, a radioactive nuclide.

radionuclide laboratory

These are laboratories listed in Annex 1 of the CTBT and include any laboratories that are certified by the IMS/IDC in the future.

real time

Actual time during which something takes place.

refline

Usually the photon line of highest intensity for a specific radionuclide. If the photon line of highest intensity has interference with another radionuclide, then the refline may be the photon line of second-highest abundance.

region of interest

Region of a radionuclide spectrum or histogram that corresponds to a particular radionuclide.

RER

Resolution (vs.) Energy Regression; an equation providing the detector-specific relationship between resolution and energy. The equation is estimated from a transmitted calibration dataset.

RERU

Resolution (vs.) Energy Regression Update. The equation contains calibration coefficients estimated from resolution-channel pairs in the current spectrum.

resolution

Metric of a detector's ability to detect photons at discrete energies and is equivalent to the FWHM; see FWHM.

RLR

Radionuclide Lab Report; report containing sample analysis results from a certified radionuclide laboratory.

RMS

Radionuclide Monitoring System; the part of the IMS that monitors the atmosphere for radionuclides originating from a nuclear weapons test.

RMSSOH

Radionuclide Monitoring System State of Health message; one of the many radionuclide data types.

RNPS

Radionuclide Network Product Summary; daily report containing a summary of the Radionuclide Network for a three-day period, including the data received, their products, and any relevant nuclides.

ROI

Region of Interest.

ROI number

Integer from 1 to 6 assigned to a 2-D ROI for the analysis of 3-D beta-gamma coincidence data.

RRR

Reviewed Radionuclide Report. Electronic file containing the final results of the analyst review of the automated radionuclide processing. It contains sections on sample information, measurement categorization, measured radionuclide quantities, MDCs, radionuclide identification, analyst editing, processing parameters, data quality flags, event screening flags, calibration equations, and field of regard.

S

s

Second(s).

sample

The solid or gaseous entity collected by a blower at an RMS station that is analyzed for its radioactive contents. This term can also refer to the automated and interactive results obtained after the acquisition of spectral data for a given sample.

sample geometry

Sample configuration, shape, and physical state in a detector chamber.

sample ID

Unique identification number assigned to a given spectrum or record by the IDC.

SAMPLEPHD

Sample Pulse Height Data; ASCII data message containing pulse height data acquired by counting a gas or particulate sample with a detector system.

schema

Database structure description.

scm

Standard cubic meter(s).

select

To choose an item on the screen by clicking it with the mouse pointer.

SID

Sample ID; unique alphanumeric string assigned to a sample during the automated processing for identification and accounting purposes.

singlet

Spectrum photopeak consisting of counts from one mono-energetic gamma ray; photopeak containing counts from multiple gamma-rays, but fit as if it is comprised of counts from only one because contributions from the individual radiations cannot be separated, as in a multiplet.

site code

Five-character alphanumeric field identifying a particular RMS site.

SOH

State-of-health.

spectral qualifier

Code in a SAMPLEPHD that indicates whether the spectrum acquisition time is truncated or full.

spectrum

A plot of the differential number of pulses (in counts) per differential pulse height (in channels or keV).

SPHD

Sample Pulse Height Data; ASCII data message type containing the pulse height data of a sample, as well as other information. The two types of SPHDs are FULL and PREL (preliminary).

SQL

Structured Query Language.

SSREB

Standard Screened Radionuclide Event Bulletin; bulletin generated by the IDC when fission or activation products are detected at a radionuclide station above normal limits. A SSREB contains information on the possible event, source location, fission products, activation products detected, any isotopic ratios calculated, and any certified laboratory results. New event information can be added to the SSREB as it arrives, therefore, multiple revisions of an SSREB are possible.

standard cubic meter

Volume occupied by $1m^3$ of gas at 0 degrees C and 1013 hPa.

station

Site where a monitoring instrument is installed.

SVD

Singular Value Decomposition.

system type

Phase of the RMS sample being collected; “P” indicates particulate and “G” gaseous.

T

total efficiency

Ratio of gamma rays interacting with the detector crystal to the total number emitted by a sample.

Trendvue

GUI-based tool that facilitates trend analysis of meteorological, station, detector, and radionuclide data.

Type I error

Spectral region of interest falsely identified as a peak by the automated processing.

Type II error

Peak undetected by the automated processing.

U

uncertainty

Best estimate of the deviation from the true mean for the parameter or variable of interest.

universal time

Absolute time using GMT as a reference.

UNIX

Trade name of the operating system used by the Sun workstations.

UPS

Uninterruptable Power Supply.

UTC

Universal Time Coordinate.

W

Web

World Wide Web; a graphics-intensive environment running on top of the Internet.

WWW

World Wide Web. The portion of the Internet that allows the display of formatted pages of text and graphics.

Y

Y

Year(s).